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US-08-232-463-14
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                                                                                                                (without alignments)
7978.235 Million cell updates/sec
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                                                                                                February 24, 2004, 02:26:33; Search time 85 Seconds
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-352-1255
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US-10-204-708-63
US-10-204-708-60
US-08-257-073-10
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US-09-508-370A-11
US-09-508-370A-11
US-09-508-370A-11
US-08-248-466B-5
US-08-257-073-15
US-08-257-073-15
US-08-257-073-15
US-08-258-370A-11
US-08-257-073-15
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                                                                                                                                                                                                                                                          682709 seqs, 277475446 residues
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                                                                       nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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BINDING PROTEINS
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                                                             697 ATTAAACGITITAAAAGAAGTGGTGATGAAAGAGAGCCGATTGTTTTCTTTGGACATGAT
                                                                                                7789 GTTIGTTTGTTTGTTGTAGTTTTGTAAATGTTTGTTTTAATGTTTTAAAGGTTATAAT
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APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE INUBERS OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
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US-08-487-826B-13/C
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
; APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
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FILING DATE: 10-SEP-1993
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ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITLE PERFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR PELING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PRILING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PELING DATE: 2000-09-01
SEQ ID NOS: 98
                                                                             GGTCAACTACCCATATGAAATATTTTTTATAAGTCCCATCCTCGAAAGTAATCCACATAT 1023
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                                                                                                                                                                                                                                 CACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAATTTTTCCTTTTTTGGCGGTAT
                                                       784 ITCCCTGAATATATATAGTACAAAAAGTCATGAGCTTATTCGCTCATGACTTTTTCGTTT
                                                                                                                                  844 AAATGATTTTTTAAATAAGTTATAAACTTTTTAGAACTATCTTCATTTAATTGATAGT
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                     Gaps
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16; Conservative 224; Mismatches 164; Indels
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llarity 43.7%; Pred. No. 0.011;
Conservative 0; Mismatches 341;
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ORGANISM: Artificial Sequence
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Best Local Simi
Matches 265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Casell, Gail H.
APPLICANT: Casell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UNCLEIC ACID PROBES AND METHOD FOR DETECTING URBAPLASMA TITLE OF INVENTION: URBALTYICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR PELING DATE: 1998-01-30
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                                  343 CCGAATCTTGAGTTCAGTGCTATTCAACAAATTCAGAAACTGGGTTTCCATCCTAAAGAT 402
                                                                                                                                 337 CTTCTTTATATTAGTTCTCACTTGCATTTTGATCATGCAGGAGGAAATGGCGCTTTT 396
                                                                                                                                                                                   403 GTGCAGCACTTTTTGTGACTCACCTCGACTTTGACCATGCGGGGGGGAATTTCAGACTTT 462
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Pred. No. 0.11;
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; ORGANISM: Ureaplasma urealyticum
US-09-601-198-60
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ilarity 47.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 15016
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Best Local Similarity
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Matches 172;
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Patent No. 6562958
GRNERAL INFORMATION:
TITLE OF INVENTION: U. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1255
LENGTH: 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081 TATCCATACTGTTAATGAATGTTTTTAATTCATCTGTTTTTGTGAGAAAGATATCCTTTT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGTCAACTACCCATATGAAATATTTTTATAAGTCCCCATCCTCGAAAGTAATCCACA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 IGICTITIGGIAGAAACIGAICGAGGCCTIGIACIGATIGAIACCGGATITGGCCTACAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 AGTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAGCAATCATCACTTCGTTACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021 TATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAATTTTCCTTTTTTGGCGG
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3.7%; Score 45.8; DB 4; Length 936;
Best Local Similarity 47.4%; Pred. No. 0.037;
Matches 137; Conservative 0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Score 48.8; DB 2; Length 1
Pred. No. 0.019;
0; Mismatches 182; Indels
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMINICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.0%;
Best Local Similarity 48.0%;
Matches 169; Conservative
                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
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US-08-487-826B-13
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 101
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 5152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31281 TTTAATAATATTCTAAAATGGCAATCACGTATATATTTTTTATATATTTTATATTTAT 31340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001098

CURRENT APPLICATION NUMBER: US/09/801,861

CURRENT APPLICATION NUMBER: 2001-03-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTGATCCTTCTTCATCTAATGTTAATTTTTCCTTTTTTGGCGGTATCCATACTGTTAAT
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APPLICANT: OLEX, Alexander
APPLICANT: PLEPENBROCK, Christian
APPLICANT: PLEPENBROCK, Christian
APPLICANT: PLEPENBROCK, Christian
APPLICANT: PLEPENBROCK, Christian
APPLICANT: PRELIN, Kurt
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PPLING DATE: 2000-04-06
PRIOR PPLING DATE: 2000-04-07
PRIOR PPLING DATE: 2000-04-07
PRIOR PPLING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                        Score 45.2; DB 4; Pred. No. 0.2; 0; Mismatches 213;
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Patent No. 6677731
                                        Sequence 3, Application US/09801861
Patent No. 6492154
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3
                                                                                                                                                                                                                                                                                              LENGTH: 53332
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US-10-204-708-73
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APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK,
APPLICANT: PREMIN Kurt
APPLICANT: BERLIN Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
TITLE OF INVENTION: by Assessing DNA Methylation
GURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DCT/PP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAGCAATCATCACTCTTCGTTACTGTG
                                                                                                                                                                                                                                                                 604 GTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTTGAAAATGAAGTGCCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        782 IGTTCCCTGAATATATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTTCGT
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                                                                                                                                                                                                   Gaps
                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4028 frririgriraggirgaaargragcgraarracggrirargara 4074
                                                                                                                                     Score 45; DB 4; Length 5152; Pred. No. 0.1; 0; Mismatches 330; Indels
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Patent No. 6677731
ORGANISM: Artificial Sequence
                                                                                                                                        Query Match
Best Local Similarity 43.4%;
Matches 255; Conservative
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ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
CITY: New York
                                                                                                                                     NAME/KEY: unsure

COCATION: (5096)

COTHER INFORMATION: n is a or g or c or

US-10-204-708-80
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US-08-257-073-10/c
; Sequence 10, Application US/08257073
...ent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA REC
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURIES, MOTTIS & S.
                       LENGTH: 8961
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   1.64; al Similarity 43.4%; 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
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     SEQ ID NO 80
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Best Local
                                                                                                                       FEATURE:
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: DIEFENBROCK, Christian
APPLICANT: DIEFENBROCK, Christian
APPLICANT: DIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
FRICK FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                              1461 TATTITAGITITAGITITITITITITITITATITITITATITITATITITATITITITITITIGITAGT 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      999 CCATCCTCGAAAGTAATCCACATATCACAGTCTATTAAAICTGATCCTTCTTCATCTAAT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITAATITITCCTITITIGGCGGTAICCATACTGTTAATGAATGTTTTTAATTCATCTGTT 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                879 GAACTATCTTCATTTAATTGATAGTACGTAAGGTTTACATCATTAGGAGTATCTTGA
                                                                                                                                                                                                                                                                                                                                                                                     819 TIAITCGCTCAIGACTITITCGTTIAAAIGALTTTTTAAAIAAGTTAIAAACTITITA
                                                                                                                                                                                                                                                                                                                                                     Gaps
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H
                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-63
                                                                                                                                                                                                                                                                                                           Length 5562;
                                                                                                                                                                                                                                                                                                           3.7%; Score 44.8; DB 4; Length 5 47.0%; Pred. No. 0.12; tive 0; Mismatches 192; Indels
Sequence 80, Application US/10204708 Patent No. 6677731
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 47.0
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1179 TGTT 1182
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-10-204-708-80
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                                                                                                                                                                                                                                                                                                                                                                          674 ATTCAGAATTAGCTTTATCTTCAATTAAACGTTTAAAAGAAGTGGTGATGAAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                    734 CGATTGTTTTCTTTGGACATGATATAGAGCAGGAAAGGGGATGTAAAGTGTTCCCTGAAT
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                    Length 8961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1094 AATGAATGTTTTTAATTCATCTGTTTTTGTGAGAAGATATCCTT 1138
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                                                                                                                                                                                                                                              Score 44.2; DB 4; Length 8 Pred. No. 0.2; 0; Mismatches 263; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/257,073
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Pohlmann, Rainer
Pohlmann, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
NVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 5181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 518
Pred. No. 0.18;
0; Mismatches 220; Indels
                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 454310-2570
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-UTN-1993
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 595, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                     FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INPORMATION:
NAME: Frommer, william S.
REGISTRATION NUMBER: 25,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.9%;
Matches 188; Conservative C
09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 5181 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic STRANDEDNESS:
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APPLICANT:
APPLICANT:
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APPLICANT:
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TTAATGAATGTTTTTAATTCATCTGTTTTTGTGAGAAAGATATCCTTTTTTGTTTTAATT 1151
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46.1%; Pred. No. 0.1;
ive 0; Mismatches 212; Indels
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATH:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: CH 0016/97
APPLICATION NUMBER: CH 0016/97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1152 GACTCGACATGTATATCTTTTATTTCTTGTTTTCCTA 1188
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                                                                      Corporation
AND USES THEREOF
                                                                 ADDRESSEE: No. 6239264artis CC
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                658 base pairs
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EDNESS: single
                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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INVENTION:
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RESULT

TITLE OF INVENTION:

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TYPE: DNA ORGANISM: Plasmodium falciparum
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                                                                                         SEQ ID NO 5
LENGTH: 10640
                                                                                                                                                                                                       NAME/KEY: CDS
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                                                   GENERAL INFUGENTION:

GENERAL INFUGENTION:

APPLICANT: DIEFENBROCK, Christian
APPLICANT: BIEFENBROCK, Christian
APPLICANT: BERLIN, Gurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: US/10/3071
PRIOR APPLICATION NUMBER: DE 10019058.6
PRIOR APPLICATION NUMBER: DE 10019058.6
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
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Patent No. 6541202
GENERAL INFORMATION:
APPLICANT: Long, David M.
APPLICANT: Maneke M.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.6%; Score 43.8; DB 4; Length 6156;
48.1%; Pred. No. 0.22;
tive 0; Mismatches 197; Indels 7
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Sequence 60, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6
Best Local Similarity 48.1
Matches 189; Conservative
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TTCGTATATTATAATACGATATTTTTTATTATTTGTAATCTTATAATTTTAAATATTT 2374
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                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (834)..(7385)
OTHER INFORMATION: TERT gene
FEATURE:
NAME/KEY: unsure
LOCATION: (1821)..(1837)
OTHER INFORMATION: a or t. Xaa (anino acid) at position 1837
OTHER INFORMATION: a or t. Xaa (anino acid) at position 330 = Leu
OTHER INFORMATION: 1le; Xaa at position 335 = Asp or Gly.
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Similarity 47.5%; Pred. No. 0.33;
72; Conservative 0; Mismatches 176; Indels
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APPLICANT: Johnson, Eric A.
APPLICANT: Bradshaw, Marite
APPLICANT: Rood, Julian
TITLE OF INVENTION: Expression System for Clostridium
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/09/417,485D
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature;
LOCATION: 3770..4013
COTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from OTHER INFORMATION: plasmid RP4"
US-09-056-075-1
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Pred. No. 0.3;
0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: 1ysyl t-RNA synthetase; OTHER INFORMATION: clone described in Example 3 US-09-508-370A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTATATCTTTATTTCTTGTTTTCCTAA 1189
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                                                            ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REPERENCE/DOCKET NUMBER: 960296.95238
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPAX: 608-251-9166
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,075
FILING DATE:
CLASSIFICATION:
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ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 50.8%;
Matches 127; Conservative
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945 ATCACTTCGTTACTGTGATGGTCAACTACCCATATGAAATATTTTTTATAAGTCCCATCC 1004
                                    1197 indaaccintircaagiaantiaaaairriaintaaaritinaaaiatinoaaaiaingacidai 1138
                                                                                                                                                   1065 TITCCITITITGGCGGTATCCATACTGTAATGAATGTTTTTAATTCATCTGTTTTTGTG 1124
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                                                                                                                                                                                                                                                                  TCGAAAGTAATCCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAAT 1064
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Job time : 98 secs
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February 20, 2004, 16:22:42; Search time 35 Seconds (without alignments) 1843.233 Million cell updates/sec
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1315
1 MTVKKLYFVPAGRCMLDHSS.....VFFGHDIBQERGCKVFPEYI 250
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_tungi:*
sp_human:*
sp_novertebrate:*
sp_mammal:*
sp_mbc:*
sp_organelle:*
sp_phage:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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Maximum DB seq length: 200000000
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sp_virus:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	0918r8 bacillus sp				, ,	O8ktw9 bacillus th		_	O8ktw6 bacillus th	_		bacilins	Osktx1 bacillus th	haciling	OSriao barillus th	bacillus
SUMMARIES	ID	Q9L8R8	QBKWS6	Q8KTW5	Q8KNY1	QBRPW5	Q8KTW9	Q8KI79	OBRPW6	Q8KTW6	Q8KTW8	Q8KTW3	Q8RPW9	Q8KTX1	O8RPW7	OBRJAO	Q8RPW4
	DB	7	~	N	~	(1	7	7	ď	7	α	7	~	~	7	~	N
	Query Match Length DB	250	250	250	250	250	250	250	250	250	250	250	250	250	250	250	250
*	Query	100.0	97.3	96.6	95.5	94.6	93.5	93.5	93.4	93.3	92.9	92.8	92.7	92.5	92.2	92.2	91.9
	Score	1315	1280	1270	1256	1244	1230	1230	1228	1227	1222	1220	1219	1216	1213	1212	1209
	Result No.	1	7	ო	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16

Q8ktw4 bacillus th				bacillus	Q8vpd5 agrobacteri	Q8ükh0 agrobacteri	Q988b9 rhizobium l	Q9wwd3 agrobacteri	Q97y13 sulfolobus	Q8kkv8 rhizobium e	Q9rh58 bradyrhizob	Q9hq42 halobacteri	028763 archaeoglob	Q978v7 thermoplasm	Q9rxy2 deinococcus		Q9pdl8 xylella fas						Q8nw27 staphylococ	Q99tb7 staphylococ	α	O92rt6 rhizobium m	Q8p8h8 xanthomonas	Q93spl plesiomonas
Q8KTW4	QBKTX0	Q8RPW8	OBRPW3	Q8KTW7	Q8VPD5	QBUKHO	Q988B9	Q9WWD3	Q97Y13	QBKKVB	Q9RH58	Q9HQ42	028763	Q978V7	Q9RXY2	Q8U664	Q9PDL8	98X8Q	Q97CB9	Q8F9T6	Q9RTE2	6MTH6O	Q8NW27	Q99TB7	Q9ALW1	Q92RT6	оврвив	Q93SP1
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91.9	91.7	91.4	91.3	91.2	24.0	23.7	22.8	22.7	19.8	19.5	19.2	19.1	18.4	18.2	17.9	17.8	16.0	14.8	14.6	14.3	14.1	14.1	14.1	14.0	13.8	13.6	13.4	13.3
1208	1206	1202	1200	1199	315	312	299.5	299	260	256.5	252	251	242.5	239.5	236	233.5	210	195	192.5	188	186	185.5	185.5	183.5	181.5	178.5	176.5	174.5
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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"Isolation of HSL lactonases and comparison of their activity against "asolation of HSL lactonases and comparison of their activity against various N-acylhomoserine lactone targets.";
Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ505742; CAD44568.1; --
InterPro; IPRO1279; Blactmase-like.
Pfan; PF00753; lactamase B; 1.
SEQUENCE 250 AA; 28179 MW; E045D41BDAA659EA CRC64;
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                                                                                                              MEDLINE=22142036, PubMed=12147491,
Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme
Widespread in Many Subspecies of Bacillus thuringlensis.";
בתבובונים tnuringiensis serovar toumanoffi.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
אלפו באווף: Bacillales (מולבים באווף) אלפונים מולבים (מולבים באווף).
אלפו באווף: Bacillales (מולבים באווף)
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EMBL, AF478058; AAM92139.1; -
InterPro; IPR001279; Blactmase-like.

Pfam; PF00753; lactmase B; 1.

SEQUENCE 250 AA; 28080 MW; 3188759211697975 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
11-ORT-2003 (TrEMBLrel. 23, Last annotation update)
N-acylhomoserine lactone lactonase.
                                                                                                                                                                                                                                                                                       96.6%; Score 1270; DB 2;
llarity 96.0%; Pred. No. 4.4e-101;
Conservative 6; Mismatches 4;
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241 KGCKVFPEYI 250
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Matches 238; Conser
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                   181 EKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQE
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Reimmann C., Ginet N., Michel L., Keel C., Michaux P.,
Rrishnapillai V., Zala M., Heurlier K., Triandafillu K., Harms H.,
Defago G., Haas D.;
"Genetically programmed autoinducer destruction reduces virulence gexpression and swarming motility in Pseudomonas aeruginosa PAOl.";
Microbiology 148:923-932 (2002).
EMBL, AR397400, AAM6172.1; -.
InterPro; IPR001279; Blactmase-like.
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Bacillus sp. A24.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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SEQUENCE 250 AA; 28010 MW; 604CF49ABBE2C386 CRC64;
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3; Mismatches
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97.2%; Pred. No. 6e
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AiiA-like protein.
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MEDLINE=22142036; PubMed=12147491;
Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Widespread in Many Subspecies of Bacillus thuringiensis.";
Appl. Environ. Microbiol. 68:3919-3924 (2002).
EMBL; AR478052, AAM92133.1;
InterPro; IPR001279, Blactmase=like.
Ffam; PF00753; lactmase=B; I.
SRQUENCE 250 AA; 28167 MW; F0BF31A687E00648 CRC64;
                                                                                                                                                                                                                                    Length 250;
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              AIIA.
Bacillus thuringiensis (subsp. kyushuensis).
Bacteria; Firmicutes; Bacillales; Bacillus.
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Bacillus thuringlensis (subsp. israelensis),
Bacillus thuringlensis (subsp. morrisoni), and
Bacillus thuringlensis (subsp. thompsoni).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
WCBI_TaxID=1440, 132264, 1430, 1441, 44162;
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Last sequence update)
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                                                                             SEQUENCE FROM N.A.
  AiiA-like protein.
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AIIA.
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21914084; PubMed=11916693;
Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
"Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTVKKLYFVPAGRCMLDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMPESAVNN
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                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus Species.",
Appl. Environ. Microbiol. 68:1754-1759(2002).
EMBL. AR350931, AAL98720.1, -.
Interpro; IRPO179; Blactmase-like.
Pfam; PF00753; lactamase B; 1.
SEQUENCE 250 AA; 28032 MW; 698589666945E1B8 CRC64;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
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Matches 232; Conservative
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MEDLINE-22142036, PubMed=12147491;
MEDLINE-22142036, PubMed=12147491;
Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
Lee S.J., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
Lee S.J., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
Lee S.J., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
Midespread in Many Subspecies of Bacillus thuringiensis.";
Appl. Environ. Microbiol. 68:3919-3924 (2002).

EMBL, ARAYSOSO, AAM92137.1;
EMBL, ARAYSOSO, AAM92137.1;
EMBL, PROVINS: Lactmase B: 1.

Pfam, PP00753; lactmase B: 1.

SEQUENCE 250 AA; 28101 WW; RDE872267R3DAD2D CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=180883;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
AilA-like protein.
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01-MAR-2003 (TrEMBLrel.
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KGCRVFPEYI 250
                                            241 KGFKVFPEYI 250
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MBDLINB=21914084; PubMed=11916693;
Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
"Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
                                                                                                                                                                                                                                                                                                                                                                             IIVQRAEYEAAQHSEEYLKECILPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET
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                                                                   93.5%; Score 1230; DB 2; Length 250; 91.2%; Pred. No. 1.2e-97; ive 15; Mismatches 7; Indels
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EMBL; AF350930; AAL98719.1; -.
InterPro; IPR001279; Blactmase-like.

Pfam; PF00753; lactamase B; 1.

PROWNGE 250 AA; 28163 MW; 12A78D220E1B2DD0 CRC64;
  Pfam; PF00753; lactamase B; 1. SEQUENCE 250 AA; 2812I MW; 1B9DC273F9CB15CF CRC64;
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Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21914084; PubMed=11916693;
Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from Bacillus Species."
Appl. Environ. Microbiol. 68:1754-1759(2002).
EMBL, PR50027; AL198716.1; -.
Interpro; IPR001279; Blactmase-like.
Pfam; PP00733; lactamase-like.
SEQUENCE 250 AA; 28084 MW; 3508246790F50709 CRC64;
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NCBI_TaxID=176903;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Last annotation update)
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
AHL-lactonase.
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                                                                                241 RGCKVFPEYI 250
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241 KGCRVFPEYI 250
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241 KGCKVFPEYI 250
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"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
Widespread in Many Subspecies of Bacillus thuringiensis.";
Appl. Environ. Microbiol. 68:3919-3924 (2002).
EMBL; AF478061; AAM92142.1;
Interprop. IPR001279; Blactmasse-like.
Pfam; PF00753; lactamase B; 1.
SEQUENCE 250 AA; 28119 MW; DFF28F553BA07C2E CRC64;
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                                                                                                                                  Query Match 92.9%; Score 1222; DB 2; Length 250; Best Local Similarity 91.2%; Pred. No. 5.8e-97; Matches 228; Conservative 14; Mismatches 8; Indels (
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Widespread in Many Subspecies of Bacillus thuringiensis.";
Appl. Environ. Microbiol. 68:3919-3924 (2002).
EMBL; AR48054; AAM92135.1; -.
Interpro; IPRO1753; lacthaase-like.
Pfam; PF00753; lacthaase B; 1.
SEQUENCE 250 AA; 28163 MW; BA2D7F09CF3F39DD CRC64;
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MEDLINE=22142036; Pubmed=12147491;
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KGCRVFPEYI 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                              MEDLINE-22142036; PubMed=12147491; Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.; Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.; Gees S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.; Medsepread in Many Subspecies of Bacillus thuringiensis."; Appl. Environ. Microbiol. 68:3919-3924(2002).

EMBL; AR478047; AAM92128.1; --
Interpro; IPR001279; Blactmass-like.

Pfam; PR00753; lactamase B; 1.

SEQUENCE 250 AA; 28003 MW; GEB53AF4A152B244 CRC64;
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NCBI_TaxID=1428, 1433, 29339, 180850;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Bacillus thuringiensis (subsp. kurstaki), and
Bacillus thuringiensis serovar indiana.
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Appl. Environ. Microbiol. 68:1754-1759(2002)
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EMBL; AF478050; AAM9213.1; -.
INLEMPRO, IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
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tes 228; Conservative
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241 KGCRVFPEYI
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STRAIN=B20, and B22;
MEDLINE=21914084; PubMed=11916693;
Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
"Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from Bacillus Species.";
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Length 250;
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90.8%; Pred. No. 4.2e-96;
cive 13; Mismatches 10; Indels
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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Last annotation update)
                                          10;
92.2%; Score 1213; DB 2; 90.4%; Pred. No. 3.4e-96;
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EMBL; AF350932; AAL98721.1; --
EMBL; AF350934; AAL98723.1; --
Interpro; IPR001279; Blactmase-like.
Pfam; PF00753; lactmase B; 1.
SEQUENCE 250 AA; 28004 WW; 6055D4F4A152B;
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241 KSCRVFPEYI 250
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Title:

Scoring table: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: Searched:

55026578

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database

em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_gss_fun:* em_gss_mam:* 1: em_estba:*
2: em_esthum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em_gss_pro:*
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			Description		AL063921 Drosophil	AL228940 Tetrandon	BX338369 BX338369	BX436282 BX436282
SUMMARIES			ID		CNS0039G		ш	BX436282
			DB	!	59	29	13	13
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ALIGNMENTS

	/c	CNS0039G 1101 bp DNA linear GSS 03-JUN-1999	Drosophila melanogaster genome survey seque	BACROBK10 of RPCI-98 library from Drosophila melanogaster (fruit	fly), genomic survey sequence.		AL063921.1 GI:4941778		Drosophila melanogaster (fruit fly)		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Ephydroidea; Drosophilidae; Drosophila.		Genoscope.	Direct Submission	L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencaqe :	BP 191 91006 EVRY cedex - FRANCE (R-mail : segref@genoscone cns_fr
RESULT 1	CNS0039G/c	LOCUS	DEFINITION			ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	TITLE	JOURNAL	

BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of tional de Sequencage

COMMENT

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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Nr. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            976 GGRKRKDKKDKKDGDDDKKGGKKKKAAAKWATKWWDDWDWDKDWKWDGAKDRKADDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 AGTIAATAATGAAGGICITITIAACGGIACAITIGICGAAGGGCAGGITITACCGAAAAI
                                                                                                                                                                                                                                                                                                                                                                              1036 WATWDTWWDKWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAATDADGAGRRD
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                                                                                                                                                                                                                                                DB 29; Length 1101;
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                                                                                                                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROBK10"
/clone="bb="RRCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                             382;
                                                                                                                                                                                                                                                 6.2%; Score 75.8; DB 29
18.7%; Pred. No. 2.5e-05;
iive 322; Mismatches 382
                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                          Conservative 322;
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 214A06 of library G from Tetraodon nigroviridis, genomic survey sequence
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CCATCCTCGAAAGTAATCCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAAT 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     856
                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigrovaridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/note="Genoscope sequence ID : C0AG214BA03SP1~end
PUC-Ori"
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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12.1%; Pred. No. 6.7e-05;
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Tetraodon nigroviridis
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BX436282.1 GI:30787521
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KEYWORDS
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                                                                                                                                                                                                                                                                                    371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX338369 1165 bp mRNA linear EST 02-MAY-2003
BX338369 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI058YF14 5-PRIME, mRNA sequence.
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857 AAATAAGITATAAACTTTTTAGAACTATCTTCATTTAATTGATAGTACGTAAGGTTTAC 916
                                                                              252 İWAAWWITATITITITAAAWITITITITITIKAAAAGGGGITTITWITITITITITITITWWWWW 311
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1165)
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIOSBDC07QP1.

Location/Qualifiers
1. .1165
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/clone lib="Homo sapiens PLACENIA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a Not!-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
                                                                                                                                                                                                                                                                                TATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAAAATGAAGTGCCATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 72.2; DB 13;
38.2%; Pred. No. 0.00013;
tive 55; Mismatches 283;
                                                                                                                                                                                                                                                                                                                                                                              1157 GACATGTATATCTTTATTTCTTGTTTTCCTAAA 1190
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/db_xref="taxon:9606"
/clone="CS0D1058YF14"
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Best Local Similarity
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BX436282 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP001YC015-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
                                                                 965 GTCAACTACCCATATGAAATATTTTTATAAGTCCCATCCTCGAAAGTAATCCACATATC 1024
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Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                  1004 WAAAAATWATATATAWAAATATATAATAWWWTWTWWAWAAAWATWAWATAWWAWTA
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                                                                                                                                             725 AAGAGAAGCCGATTGTTTCTTTGGACATGATATAGAGCAGGAAAGGGGATGTAAAGTGT
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BP 191 91006 BYRY cedex - France
Email: seqreségenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invircogen. Contact : Feng Liang Email : fliang@lifetech.com U
http://fulllength.invirtogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAFOOlABOlQP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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CD386564 1067 bp mRNA linear EST 30-MAY-2003
AGENCOURT_14286445 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
CD386564
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1067)
                                                                                                                                                                                                                                                                /day stages adult.../lab host-models (phage-resistant)" /lab host-models (phage-resistant)" /lab host-models (phage-resistant)" /lone lib="NutUD XGC Eyel" /note="Organ: eye; Vector: pCWV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo of Average insert size 2.3 kb. Constructed by Life Average insert size 2.3 kb. Constructed by Life (Exchologies. Note: This is a Xenopus Gene Collection (XGC) library."
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM4564 row: o column: 14
High quality sequence start: 49
High quality sequence stop: 150.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 68.6; DB 14;
48.3%; Pred. No. 0.00071;
tive 0; Mismatches 225;
                                                                                                                                                                                             /organism="Xenopus laevis"
                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6949287"
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Best Local
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniels Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloA07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                      697 ATTAAACGTTTAAAAGAAGTGGTGATGAAAGAGAAGCCGATTGTTTTCTTTGGACATGAT
         the pCMVSPORT 6 vector
                                                                                                                           1;
                                                                                      DB 13; Length 1124;
                                                                                                                           Indels
                                                                                      5.9%; Score 72; DB 13; L
larity 27.4%; Pred. No. 0.00015;
Conservative 157; Mismatches 240;
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Eukaryota; Metazoa; Chordata; Craniata;
             Not I and EcoRV sites of rary was not normalized."
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Best Local Similarity
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                                                Contact: Daniela (157)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M. AG.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: NDKW74 row: e column: 02
High quality sequence start: 8
High quality sequence start: 8
High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_173"
/note="Vector: pDONE201; Site_1: attp2; Site_2: attp1;
LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
LIBR_PROVIDER - Bradfield"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
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All Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoll Ecoll digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland BSC libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://www.iff.com.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                               CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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688 ITATCITCAAITAAACGITTAAAAGAAGIGGIGAIGAAAGAAGACGAAIIGIIJITCITI
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/organism="Drosophila
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/note="end : TET3"
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Genoscope...
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
Submitted (02-JUN-1999) Genoscope - FRANCE (E-mail : segref@genoscope.cns.fr
      ATATTTGAAAGAATGTATATTGCCGAATTTAAACTACAAAATCATTGAAGGTGATTATGA
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/dev_ctage="fetal"

/cone lib="Homo sapiens FETAL BRAIN"

/note="Organ: Drain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and BCORV sites of the pCMVSPORT 6

vector. Library was not normalized."
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF005BH09NP1.
Location/Qualifiers
AAACTTTTTTAGAACTATCTTCATTTAATTGATAGTACGTAAGGTTTACATCATTAGGAG
                   AAYYYYYTCMYYYHYMHMHAHAHAHAAAAWWTTHTWWTHAYHWATYHYYYXWYCAMMCMCTH
                                                                TATCTTGTTGAGCAATCATCACTTCGTTACTGTGATGGTCAACTACCCATATGAAATATT
                                                                                   CITCATCIAAIGITAAITITCCITTTTTGGCGGTAICCATACTGTAAIGAAIGITTTTA
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BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="FETAL BRAIN"
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/clone="CS0DF005Y018"
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Mammalia; Eutheria; Primates;
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1101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
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                                 AGTCGTACCAGGAGTTCAATTATTGCATACACCAGGCCATACTCCAGGGCATCAATCGCT
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 1101)
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Homo sapiens
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer centeries at the Roswell Park Cancer institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 66.8; DB 29;
; Pred. No. 0.0016;
94; Mismatches 286;
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/note="end : T7"
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BX335216

RESULT

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BX335216 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA colone CS0DI012YG10 5-PRIME, mRNA sequence.
                                        EST 02-MAY-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotLoligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sites of the pCMVSPORT 6 vector, Library was normalized,
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cgi-bin/cluster.cgi?seq=CSODI012BD05QP1&cluster=714.f. Contact
cgi-bin/cluster.cgi?seq=CSODI012BD05QP1&cluster=714.f. Contact
Feng Liang Fmail: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI012BD05QP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
BMail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 714.f.
more information about this cluster, see
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                                                                                                                                                                                                                                                                                                                                                                                    i. W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CS0D1012YG10"
                                                                                                                                                                  BX335216.1 GI:30341402
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Ly Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux. CP 5706, 91057 EVRY cedex - FRANCE (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrocmyca marxianus var. setting sorbitophila, Candida tropicalis and Yarromyca (Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                        S07ABZ 897 bp DNA linear GSS 08-JUL-2001 end of clone BC0AA003A12 of library BC0AA from strain CBS 767 of
TICATCIGITITIGIGAGAAAGATAICCITITITIGITITAATIGACICGACAIGTAIAIC 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Dujon, B., Durens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.

1 (bases 1 to 897)
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PEBS Lett. 487 (1), 82-86 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                          Debaryomyces hansenii (anamorph: Candida famata)
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/organism="Debaryomyces hansenii"
/mol_type="genomic DNA"
/strain="CBS 767"
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/clone="BC0AA003A12"
/clone_lib="BC0AA"
/note="end : T7"
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GSS.
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PUBMED
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5.4%; Score 66.4; DB 29; Length 897;

Query Match

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/tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dI) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Genoscope - Centra National de Sequencage
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact. : Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP004AD10NP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                    819 TTATTCGCTCATGACTTTTTCGTTTAAATGATTTTTTAAATAAGTTATAAACTTTTTA
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il Similarity 45.6%; Pred. No. 0.0021;
178; Conservative 13; Mismatches 199; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone="CS0CAP004YG19"
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1168 RKWIDIAAAAAWWKIIKIKKIKKIKITWITAIWTITITKIKIKIKITITKIAAWAAAAA 1109
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981 bp mRNA linear EST 15-MAY-2003
BX425658 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
    580 ATTGAGACAGAAAATCCGGTCCTGTATTATTAACGATTGATGCATCGTATACGAAAGAG 639
                                                                                               640 AATTITGAAAATGAAGTGCCATTTGCGGGATTTGATTCAGAATTAGCTTTATCTTCAATT 699
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                    700 AAACGITIAAAAGAAGIGGIGAIGAAAGAGAAGCCGAIIGITITICITIGGACAIGAIAIA
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                     1024 CACAGTCTATTAAATCTGATCCTTCTTCAATGTTAATTTTTCCTTTTTTGGCGGTAT 1083
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                                                                                                                                                                                /tissue type="NEUROBLASTOMA COT 25-NORMALIZED" /clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and cloned into the Not I and ECRY sites of the pCMVSPORT 6 vector. Library was normalized."
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10493.f For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                             844 AAATGATTTTTTAAATAAGTTATAAACTTTTTTAGAACTATCTTCATTTAATTGATAGT
                                                                                                                                  904 ACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAGCAATCATCACTTCGTTACTGTGAT
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    Gaps
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODC029CH02QPI.
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  59; Mismatches 163; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="CLOBB024ZHO7"
/tisue_rype="NBUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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1. (Dases 1 to 1200)

1. (M.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDPA, libraries and normalization

Unpublished (2001)
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5393.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP002AF05QP1&cluster=5393.f. Contact
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Feng Liang Email : fliang@lifetech.com URL :
http://fullIngth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP002AF05QP1.
Location/Qualifiers
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/ISO6_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/ISO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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Perfect :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* Query

Description	Sequence 2, Appli	Sequence 57885. A	Sequence 1, Appli	Sequence 240, App	Sequence 1931, Ap	Sequence 5785, Ap	Sequence 33, Appl	Sequence 299, App	Sequence 1497, Ap	Sequence 2128, Ap	Sequence 95, Appl	Sequence 107. App	Sequence 654, App	Sequence 150, App	GENERAL INFORMATI
ID	14 US-10-312-841-2		14 US-10-312-841-1	4 US-10-311-455-240	4 US-10-311-455-1931	US-09-960-352-5785	2 US-10-221-613-33	4 US-10-311-455-299	4 US-10-311-455-1497	4 US-10-311-455-2128	4 US-10-239-676-95	4 US-10-240-453-107	4 US-10-311-455-654	6 US-10-257-166-150	6 US-10-211-179-11
Query Match Length DB ID	4.9 3673778		1.6 3673778	6419 1	14006 1	516 9	6109 1	6109 1	6035 1	15548 1	15732 1	15732 1	6436 1	8776 1	.3 158001 1
Query Match	4.9	4.7	4.6	4.5	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.3	4.3	4.3
Score	59.8	57.8	26	55.6	55.6	54.8	54.8	54.8	53.4	53.4	53.2	53.2	53	53	52.8
Result No.	7	7	m	4	ស	9	7	σο	σ	10	11	12	13	14	c 15

Sequence 52, Appl	Sequence 54, Appl	Sequence 16, Appl	Sequence 3400, Ap	Sequence 39, Appl	Sequence 1053, Ap	79	Sequence 14, Appl	22	16	Sequence 1304, Ap	986		51	53	13	94	12	Sequence 141, App	34	Sequence 1746, Ap				Sequence 14, Appl	Sequence 95, Appl		Sequence 7, Appli	Sequence 384, App	1366,
US-10-239-676-52	US-10-240-453-54	US-10-221-613-16	US-09-960-352-3400	US-10-221-613-39	US-10-311-455-1053	US-10-240-485-79	US-10-239-676-14	US-10-240-453-22	US-10-311-455-1692	US-10-311-455-1304	US-10-311-455-986	US-10-311-455-1981	US-10-239-676-51	US-10-240-453-53	US-10-239-676-132	US-10-311-455-945	US-10-239-676-121	US-10-240-453-141	US-10-257-166-34	US-10-311-455-1746	US-10-311-455-1944	US-10-311-455-336	US-10-240-485-30	US-10-240-452-14	US-10-257-166-95	US-10-311-455-131	US-10-240-452-7	US-10-311-455-384	US-10-311-455-1366
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4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1
52.6	52.6	52.6	52.4	52.4	52.2	52.2	52.2	52.2	52	51.8	51.6	51.4	51.4	51.4	51.2	51.2	51.2	51.2	51	50.8					50.4	50.4	50.4	50.2	50.2
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION WUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1064838 TTTAGTGAAATAGTAAATGATATTATGATTTAATATATAATTTAATTTAATTATAAGTATT 1064897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59.8; DB 14; Length 3673778; Pred. No. 0.24; 0; Mismatches 227; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                  ; Sequence 2, Application US/10312841; Publication No. US20030186277A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.3%;
Matches 196; Conservative (
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2
                                                                                                                                                                                                                                                                              LENGTH: 3673778
US-10-312-841-2
                                                                                                                                                                                                                                                      SEQ ID NO 2
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663

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
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663 IGCGGGATITGATICAGAATIAGCITTAICTICAATIAAAACGITTAAAAAGAAGIGGIGAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6%; Score 56; DB 14;
44.8%; Pred. No. 1.6;
tive 0; Mismatches 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: chemically treated genomic
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
                                                                                                                                                                                                  ; Sequence 1, Application US/10312841; Publication No. US20030186277A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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LOCATION: (3294164)
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Matches 215;
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US-10-312-841-1
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US-10-312-841-1
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                      CCATCCTCGAAAGTAATCCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAAT 1058
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            TATGAAATATTTTTTATAAGTCCCATCCTCGAAAGTAATCCACATATCACAGTCTATTAA 1036
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4.7%; Score 57.8; DB 12; Length
Best Local Similarity 47.3%; Pred. No. 0.0094;
Matches 173; Conservative 0; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_23282C.1 US-10-424-599-57885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(673)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-57885
; Sequence 57885, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
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LOCATION: (1)..(6
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Gaps

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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND CHHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5785
LENGTH: 516
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                                                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 0.13;
0; Mismatches 194; Indels
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; LOCATION: (76), (90)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1

US-09-960-352-5785
                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: 8289, 8310, 8313
OTHER INFORMATION: n is a or g or c or
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                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.0%;
Matches 172; Conservative
  PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1931
LENGTH: 14006
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US-09-960-352-5785
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               APPLICANT: BERLIN, Kutt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
FITLE OF INVENTION: Oytosine methylation
FILE OF INVENTION: Oytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: US/10/311,455
PRIOR FILING DATE: 2002-12-16
PRIOR PELING DATE: 2001-07-02
PRIOR FILING DATE: 2000-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 240
LENGTH: 6419
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: OLO-12-16
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT PILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: DE 10032529.7
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Pred. No. 0.087;
0; Mismatches 214; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-240
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Publication No. US20030143606A1
PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.5%;
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Best Local Similarity 47.6°
Matches 195; Conservative
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Mur
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: cytosine methylation
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NOS: 2424
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                                                                        895 ATTGATAGTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAGCAATCATCACTTCGT
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47.2%; Pred. No. 0.13;
tive 0; Mismatches 187;
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TTTTCGTTTAAATGATTTTTTTAAATAAGTTATAAACT
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LOCATION: 214, 2796..2797, 4347

COTHER INFORMATION: n is a or g or c or

US-10-311-455-299
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Matches 167; Conservative
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GENERAL INFORMATION:
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US-10-311-455-299
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publication No. US20040029123A1

publication No. US20040029123A1

publication No. US20040029123A1

publication No. US20040029123A1

publication No. US20040029123A1

APPLICANT: OLEK, ALexander

APPLICANT: DIEPENBROCK, Christian

APPLICANT: DIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TILLE OF INVENITON: Diagnosis of Diseases Associated with Cell Cycle

FILE REFERENCE: 5013.1004

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: PCT/EP01/02945

DE 100193847.00

DE 10019058.8

DE 10019058.8

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PRIOR PILING DATE: 2001-03-15

PRIOR PILING DATE: 2001-03-15
                                                                                  793 TATATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTTCGTTTAAATGATTT
                                                                                                                                                                                                    retriatadaguriaaatricriaanggcaataaggratngagggriagirirnatarrir
                                                                                                                                                               853 TITIAAAIAAGITAIAAACITITITAGAACIAICITCAITIAAITGAIAGIACGIAAGGI
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4.5%; Score 54.8; DB 12; Length 6109;
Best Local Similarity 47.2%; Pred. No. 0.13;
Matches 167; Conservative 0; Mismatches 187; Indels 0;
      Length 516;
    Score 54.8; DB 9; Length 5
Pred. No. 0.038;
0; Mismatches 214; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEX: unsure
; LOCATION: (214, 2796..2797, 4347)
0S-10-221-613-33
  4.5%;
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ORGANISM: Artificial Sequence
      Query Match
Best Local Similarity 46.08
Matches 182; Conservative
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SEQ ID NO 33
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2000-06-30
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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEBENBROKCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
FRIOR PELICATION NUMBER: PCT/EP01/07537
FRIOR PELICATION NUMBER: DE 10032529.7
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR THING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SCO ID NO 2128
FUNDER OF SEQ ID NOS: 2424
FUNDER OF SEQ ID NOS: 2424
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Fublication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: BIELIN, Kurt
ITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT APPLICATION NUMBER: PCT/EP01/03968
DE 10019059.8
DE 10019059.8
DE 10019059.8
DE 10032529.7
DE 10032529.7
SPIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.4%; Score 53.4; DB 14; Length 15548; larity 46.8%; Pred. No. 0.41; Conservative 0; Mismatches 191; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
        Publication No. US20030143606A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BEELIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10035529.7
PRIOR APPLICATION NUMBER: DE 10035529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1497
                                                                                                                                                            2040
                                                1075 TGGCGGTATCCATACTGTTAATGAATGTTTTTAATTCATCTGTTTTTGTGAGAAAGATAT 1134
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ICCACATATCACAGICIATIAAATCIGAICCTICTICAICIAATGITAATITITCCTTTTT 1074
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                                                                                                                                                    1981 GGTTTATTTATTTATTTATTTATTTATTTATTTATATATTTATTTATTTATTTATT
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46.8%; Pred. No. 0.25;
tive 0; Mismatches 191; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1497, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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US-10-311-455-2128
: Sequence 2128, Application US/10311455
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Best Local Similarity 46.8
Matches 168; Conservative
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2000-04-06

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Sequence 654, Application US/10311455
; Sequence 664, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
    APPLICANT: OLEK, Alexander
; APPLICANT: DIEK, Alexander
; APPLICANT: DIEK, Alexander
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
; TITLE OF INVENTION: US4002-12-16
; TITLE OF INVENTION: UNMER: VS/10/311,455
; CURRENT APPLICATION NUMBER: PCT/EP01/07537
; FILE REFERENCE: 2002-02-12-16
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 654
; LENGTH: 6436
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                                                                                                                                                                                                                                                                                              855 TIAAATAAGTTATAAACTTTTTAGAACTATCTTCATTTAATTGATAGTACGTATT
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-654
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H
                                           OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                              Length 15732
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4.3%; Score 53; DB 14; Length 64.

Best Local Similarity 45.8%; Pred. No. 0.32;

Matches 182; Conservative 0; Mismatches 215; Indels
                                                                                                         Score 53.2; DB 14; Length Pred. No. 0.45; 0; Mismatches 208; Indels
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                                                                                                              # 4.4%;
Best Local Similarity 47.5%;
Matches 189; Conservative (
ORGANISM: Artificial Sequence
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US-10-311-455-654
                                                                     US-10-240-453-107
                            FEATURE:
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by Means of Assessing the Methylation Status of Genes Associated
With DNA TRanscription
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PUBLICARY APPLICATION US/10240453

PUBLICARY OLEX, Alexander

APPLICANT: DIEFENBROCK, Christian
APPLICANT: DIEFENBROCK, Christian
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APPLICANT: DIEFENBROCK, Christian
APPLICANT: DIEFENBROCK, Christian
APPLICANTON: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: DY Means of Assessing the Methylation Status
TITLE OF INVENTION: DY MEER: US/10/240,453
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT APPLICATION NUMBER: DE 1001973-8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 1001973-8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350

LENGTH: 15732
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                                                                                                                                                                                           OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                              Length
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Pred. No. 0.45;
0; Mismatches 208;
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Best Local Similarity 47.5%;
Matches 189; Conservative (
                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                         228
                                    2000-09-01
NUMBER OF SEQ ID NOS:
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                                                                                                     LENGTH: 15732
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                                                                            SEQ ID NO 95
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Best Local Similarity 43.2%;
Matches 252; Conservative
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Job time : 1456 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 150, Application US/10257166
Publication No. US20040023230A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
                                                                                                                                                                                          TTAAATCTGATCCTTCTTCATCTAATGTTAATTTTTCCTTTTTTTGGCGGTATCCATACTGT 1092
                                                                                                                                                                                                                                                                                        TAATGAATGITITITAATICATCTGITITITGTGAGAAGATAICCTTTTTTGTTTAATIG 1152
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TATTTATTATTAAATTATTTTTTATTATTTTAAGACGTTATTGATTTTATAATTTATTA 3059
                                                              TITIAATITATTATTATAAGITAGAAAAATGIGATATATTAATGATTGTAAGAAATAT 3119
                                                                                                                            TTTAATTTTAGGGTTATGAAGAAAGGTATTTTAGAATTAATGAAATATAGTGGAAAATA 3179
                                                                                                                                                            CCCATATGAAATATTTTTATAAGTCCCATCCTCGAAAGTAATCCACATATCACAGTCTA 1032
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                               TITIAAATAAGITATAAACITITIAGAACIATCITCATITIAATIGATAGIACGIAAGGI
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4.3%; Score 53; DB 16; Length 87
Best Local Similarity 46.8%; Pred. No. 0.37;
Matches 167; Conservative 0; Mismatches 190; Indels
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: PCT/EPO1/07470
DE 10033529.7
DE 10043826.1
PRIOR FILING DATE: 2001-06-29
2000-06-30
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ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 150
LENGTH: 8776
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APPLICANT: Nicholas M. Dean
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI-
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI-
CURRENT APPLICATION NUMBER: US/10/211,179
CURRENT APPLICATION NUMBER: US/10/211,179
CURRENT FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 119
US-10-211-179-11
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7032 TAATAAGTTAAGATTTGGTTATTAAGTGTGTTTATTGTTATTGAAATGTTATTGTTATTT 7091
                                                                 TTTTGGCGGTATCCATACTGTTAATGATGTTTTTAATTCATCTGTTTTTGTGAGAAAGA 1131
                                                                                                                              907
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Run on:

February 24, 2004, 01:02:27; Search time 415 Seconds (without alignments) 12509.152 Million cell updates/sec

US-10-019-661-1 Title: Perfect score:

1 ctttactgtattgtttttttt......tcatttgggtctctttgagt 1222 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* N Geneseq_29Jan04:* genesegn1980s:* genesegn1990s:* geneseqn2000s:* Database

Result No.

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ALIGNMENTS

Listeria sp. strain 240B1 aiiA gene. AAF29642 standard; DNA; 1222 BP. (first entry) 10-APR-2001 AAF29642; AAF29642 RESULT 1 8×4×4×8

ia; ailà; autoinducer inactivation protein A; antibacterial; e resistance; soft rot disease resistance; bacterial infection; ds.

ia sp.

02578-A1

.2001.

99WO-SG000128. -1999; 99SG-00003146. -1999;

INST MOLECULAR AGROBIOLOGY 1 RES LINK.

ii Z, Yihu D, Jinling X;

001-138146/14. AAB50476 cterial autoinducer inactivation proteins and nucleic acids my the protein, for increasing disease resistance, preventing or my bacterial damage to a plant or animal, or treating bacterial ions in animals.

2; Fig 4A; 49pp; English.

The present sequence is a nucleic acid encoding a bacterial autoinducer inactivation protein (AiiA). It is useful for increasing disease resistance as well as preventing or reducing bacterial damage to a plant or animal. The nucleic acid may be used to confer resistance to diseases where expression of pathogenic genes are regulated by autoinducers, such as diseases caused by Pseudomonas aeruginosa, Erwinia stewatii, Xenorhabdus nematophilus, Erwinia chrysanthemi, Pseudomonas solanacearum and Xanthomonas campestris. It may also be used to confer soft rot disease resistance in susceptible plants such as potato, eggplant,

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The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance to a disease in sustainable plant or animal and for reducing bacterial damage.
          GATGGTCAACTACCCATATGAAATATTTTTTTAAAGTCCCATCCTCGAAAGTAATCCACA
                                                                                 TATCCATACTGTTAATGAATGTTTTTAATTCATCTGTTTTTGTGAAAGATATCCTTTT
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                          GATGGTCAACTACCCATATGAAATATTTTTTATAAGTCCCATCCTCGAAAGTAATCCACA
                                                                TATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAATTTTTCCTTTTTTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autoinducer inactivation, AilC; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora; gene; ds.
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/note= "Autoinducer inactivation protein"
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carrot and celery. The bacterial autoinducer ein may be directly used to treat or prevent
                                                         Sequence 1222 BP; 376 A; 180 C; 238 G; 428 T; 0 U; 0 Other;
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larity 100.0%; Pred. No. 5.8e-251;
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    Chinese cabbage, carrot a inactivation protein may
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The invention describes an isolated polynucleotide encoding
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biofilm-forming bacteria to the autoinducer inactivation protein. A blacterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This sequence encodes the autoinducer inactivation activity of which is studied in the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                             Score 1037; DB 6;
Pred. No. 1.6e-211;
0; Mismatches 115;
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                                                                                                                                                                                                                              ATGGTCAACTACCCATATGAAATATTTTTTATAAGTCCCATCCTCGAAAGTAATCCACAT
                                                                                                   GTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAGCAATCATCACTTCGTTACTGTG
                                                                                                                                                           Graceradaritracarcaccaeraricriscristicarcarcarregistracians
                                                                                                                                                                                                                                                                  ATGATCAACTACCCATATGAAAATATTTTTTATAAGTACCATCCTCAAATGTAATCCACAT
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                                                                                                                                                                                                                                                                                                                                                                                                   ATCACAATCTATTAAATCTGATCCTTCTTCATCTAATGTTAATTTTCCTTTTTTGGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AICCATACTGTTAATGAATGTTTTTAATTCATCTGTTTTTTGTGAGAAAGATATCCTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autoinducer inactivation, AiiG; N-acyl-homoserine lactone, disease resistance; bacterial damage reduction; biofilm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "AiiG"
/note= "Autoinducer inactivation protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soft rot disease; Erwinia carotovora; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding autoinducer inactivation protein AiiG
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RESULT 4

ABK4747

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polymucleotide is useful for increasing disease resistance in a plant or animal by introducing a polymucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human, and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A bacterial cell transformed with the polymucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B21 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This sequence encodes the autoinducer inactivation protein AiG, the autoinducer inactivation activity of which is studied in the invention. (Updated on 29-AUG-2003 to standardise OS field)
inactivation protein.
   (N-acyl-homoserine lactone)
      autoinducer
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Sequence 753 BP; 243 A; 108 C; 172 G; 230 T; 0 U; 0 Other;

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                                                                                                         1 ATGACAGTAAAGAAGCTTTATTTCGTCCCAGCAGGTCGTTGTATGTTGGATCATTCGTCT
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   Length 753;
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Query Match 52.7%; Score 644.2; DB 6; Best Local Similarity 91.0%; Pred. No. 7.8e-128; Matches 685; Conservative 0; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance to a disease in sustainable plant or animal and for reducing bacterial damage.
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                                                                                                                                                                     Autoinducer inactivation; AilF; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora; gene; ds.
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ABK47471 standard; DNA;
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18-JUN-2002
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Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance to a disease in sustainable plant or animal and for reducing bacterial damage.
                                                                  (MOLE-) INST MOLECULAR AGROBIOLOGY
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                                               23-AUG-2000; 2000WO-SG000123
                                                                                     Zhang L, Dong Y, Xu
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P-PSDB; AAU78806.
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0; Mismatches 81;
Claim 4; Fig 9; 82pp; English.
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672; Conservative
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ABK47474 standard; DNA; 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for inoreasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably
                                       540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance to a disease in sustainable plant or animal and for reducing bacterial damage.
TGTATATTACCGCATTTGAACTACAAATTATTGAAGGGGATTATGAAGTGGTACCAGGT 480
                                GATGAAGTGCCGTTCGCAGGATTTGATCCAGAATTAGCTTTATCTTCAATTAAACGTTTA
                                                                                                                                            AAAGAAGTGGTGATGAAAGAGAAGCCGATTGTTTTTTTTGGACATGATATAGAGCAGGAA
                                                                                                                                                         GAGCAATCCGGTTCAGTTTTATTAACGATTGATGCATCGTACACGAAAGAAGAATTTTGAA
                                                                                                     649 AATGAAGTGCCATTTGGGGGATTTGATTCAGAATTAGCTTTATCTTCAATTAAACGTTTA
                    GTTCAATTATTGCATACACCAGGCCATACTCCAGGGCATCAATCGCTATTAATTGAGACA
                                                           GAAAAATCCCGGTCCTGTATTAATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAA
                                                                                                                                                                                                                                                                                                                                                 Autoinducer inactivation, AiiD; N-acyl-homoserine lactone, disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Autoinducer inactivation protein"
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(first entry)
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human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A bacterial cell transformed with the polymucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This sequence encodes the autoinducer inactivation protein AiiD, the autoinducer inactivation activity of which is studied in the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                     Score 620.2; DB 6;
Pred. No. 1e-122;
0; Mismatches 83;
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Best Local Similarity 89.0%;
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/note= "Autoinducer inactivation protein"
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(Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                     Autoinducer inactivation, AilI; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora; gene; ds.
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/product= "AilI"
/note= "Autoinducer inactivation protein"
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88.7%; Pred. No. 4.9e-122;
tive 0; Mismatches 85;
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                                                                                    (first entry)
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                                                                  (revised)
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P-PSDB; AAU78810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 617; DB 6; Length 75
Pred. No. 4.9e-122;
0; Mismatches 85; Indels
                           (MOLE-) INST MOLECULAR AGROBIOLOGY
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23-AUG-2000; 2000WO-SG000123.
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                                                    Dong Y, Xu
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The invention describes an isolated polynuclectide encoding an autoinducer (Nacyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human, and for reducing the formation of bacterial biofilums, by exposing biofilum-forming bacteria to the autoinducer inactivation protein. A bacterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from Bl. B2, B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
                                                                                                                708
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GAAAAATCCGGTCCTGTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAA
                                 AATGAAGTGCCATTTGCGGGATTTGATTCAGAATTAGCTTTATCTTCAATTAAACGTTTA
                                                                                                                                                                       Autoinducer inactivation; AilJ; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora; gene; ds.
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/product= "AiiJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
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P-PSDB; AAU78811.
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Autoinducer inactivation; AiiK; N-acyl-homoserine lactone;

encoding autoinducer inactivation protein AiiK

disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora; gene; ds.

Location/Qualifiers

Bacillus thuringiensis;

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/note= "Autoinducer inactivation protein"

/product= "AiiK"

WO200216623-A1

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(MOLE-) INST MOLECULAR AGROBIOLOGY

23-AUG-2000; 2000WO-SG000123.

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 in a susceptible plant or animal, where virulence is regulated by
                                                                                                                                                                                                                    09
              autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This sequence encodes the autoinducer inactivation protein AilJ, the autoinducer inactivation activity of which is studied in the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                           61 GTTAATAGTACACTCGCGCGGGAATTTATTGAACTTACCTGTATGGTGTTATCTTTTG
                                                                                                                                                                                                                                                                                                           GAGACTGAAGAAGGACCTATTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAAT
                                                                                                                                                                                                                                                                                                                             121. GAGACAGAAGAGGGCCTATTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAAT
                                                                                                                                                                                                                                                                                                                                                                                             GATAGAATCGTGAATATTTTAAAACGGGTTGGTTATGAGCCGGAAGACCTTTTATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 ATTAGTICICACTIACATTITGATCATGCAGGAAACGGTGCTTTTACAAATACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTATATTGCCGAATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGA
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                                                                                                                                                                                                                                                                                                                                                                          GAAGGTCTTTTTAACGGTACATTTGTCGAAGGGCAGGTTTTACCGAAAATGACTGAAGAA
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                                                                                                                                                                                                                  1 ATGACAGTAAAGAAGCTTTATTTCATCCCAGCAGGTCGTTGTATGTTAGATCATTCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                        0;
                                                                                                                        Length 753;
                                                                                           Sequence 753 BP; 234 A; 111 C; 177 G; 231 T; 0 U; 0 Other;
                                                                                                                                                       Indels
                                                                                                                                                       86;
                                                                                                                          DB 6;
                                                                                                                       Score 615.4; DB 6
Pred. No. 1.1e-121
0; Mismatches 86
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                                                                                                                        50.4%;
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Best Local Similarity
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Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance to a disease in sustainable plant or animal and for reducing bacterial damage.
                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTAATGGTACACTCGCGCCGGGGAATTTATTGAACTTACCTGTATGGTGTTATCTTTTG
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Pred. No. 2.4e-121;
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                                                                                                                                                                                                                                                      Zhang
                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.2%;
                                                                                                                                                                                                                                                       Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666; Conservative
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Best Local Similarity
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ABK47476 standard; DNA; 753

(first entry)

(revised)

29-AUG-2003 18-JUN-2002

ABK47476;

RESULT 10
ABK47476
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181 GAAGGGCTTTTTAACGGTACATTTGTTGAAGGACAGATTTTACCGAAAATGACTGAAGAA 240
                                                                                                                                                                                                                                                                                               241 GATAGAATCGTGAATATATATAAGCGTGTAGGGTATGAGCCGGACGACGACCTTTTATATAT
                                                                                                   301 ATTAGTICICACTIACATITIGATCATGCAGGAGGAAACGGTGCTTTTACAAATACACG
                                                                                                                                                 TGTATATTGCCGAATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGA
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                         GATAGAATCGTGAATATTTTAAAAOGGGTTGGTTATGAGCCGGAAGACCTTCTTATATT
                                                                           ATTAGTTCTCACTTGCATTTTGATCATGCAGGAGGAAATGGCGCTTTTATAAATACACCA
                                                                                                                             TGTATTACCGCATTTGAACTACAAATTATTGAAGGGGATTATGAAGTGGTACCAGGT
                                                                                                                                                                                                                                                                               GAAAAATCCGGTCCTGTATTAATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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3, Lesche R, Leu E;
Mueller V, Otto T, )
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P, Grabs (
Model F, 1
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Piepenbrock C, Adorjan
Lipscher E, Maier S,
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Detecting and differentiating between hematopoietic cell proliferative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                           The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAATTTTCCTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders allowing for improved and informed treatment of patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score 57; DB 7; Length 8056;
.larity 47.4%; Pred. No. 0.017;
Conservative 0; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                         Claim 28; SEQ ID NO 386; 117pp; English
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Matches 171; Conserv
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with consultation of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences (CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid conjugement (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single conjugement (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for accertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences confirmed from tumour suppressor genes and oncogenes. Sequences with even compared seq 1D numbers are the complementary sequence of the numbered seq 1D numbers are the complementary sequence of the numbered seq 1D numbers are the complementary sequence of the number of the sequences and oncogenes. Sequences with the number of the sequences of the complementary sequence of the number of the sequences of the complementary sequence of the number of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complementary sequence of the sequences of the complem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 56; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                      2000DE-01019058.
2000DE-01019173.
2000DE-01032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                  WO200168912-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000;
30-JUN-2000;
                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000;
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                                                                                                                                                                                                                                           20-SEP-2001
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Sequence 7667 BP; 2292 A; 63 C; 1436 G; 3876 T; 0 U; 0 Other;

ò. 4644 4704 820 TATTCGCTCATGACTTTTTCGTTTAAATGATTTTTTTAAATAAGTTATAAACTTTTTTAG TATITITITAGITITATITITAAAATITITITATITIGAATITITATITIAGATT 940 CAATCATCACTTCGTTACTGTGATGGTCAACTACCCATATGAAATATTTTTTATAAGTCC 880 AACTATCTTCATTTAATTGATAGTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAG Gaps . 0 Score 56.6; DB 4; Length 7667; Pred. No. 0.021; 0; Mismatches 199; Indels 0; 4.6%; Matches 176; Conservative Query Match Best Local Similarity 4585 1645

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention

Claim 1; SEQ ID NO 240; 32pp + Sequence Listing; German.

methylation.

Sequence 6419 BP; 1565 A; 53 C; 1453 G; 3348 T; 0 U; 0 Other;

ij

Gaps

1;

Length 6419; Indels

Score 55.6; DB 6; Pred. No. 0.033; 0; Mismatches 214;

Query Match
Best Local Similarity 47.6%;
Matches 195; Conservative

4884 1000 CATCCTCGAAAGTAATCCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATG 1059 TITATITITGAAATAITITGIGITITITAAATTATITGATITGITATATITITAT 4944 antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective, anti-HIV, anticonvulsant, ophthalmological; neuroprotective, antia-HIV, anticonvulsant, antipsoriatic, antithelamatory, cancer, eye disease, arteriosclerosis, anaemia, acute myeloid leukaemia, Albeimer's disease, AIDS; epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis; bowel disease; gene, Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine 1120 TIGIGAGAAAGATATCCTITITIGTTTTAATTGACTCGACAIGTATATCTTTTATTTCTT system disease; cytosine methylation; antiasthmatic; Human immune system associated gene SEQ ID NO: 240. Berlin K; BP 4945 TTTTTTTAATAGA 4959 1180 GITTTCCTAAAAGA 1194 ABL32267 standard; DNA; 6419 02-JUL-2001; 2001WO-EP007537. 2000DE-01032529 2000DE-01043826 (first entry) Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2002-130909/17 WO200200928-A2 Homo sapiens 30-JUN-2000; 01-SEP-2000; 26-MAR-2002 03-JAN-2002. 1060 4825 4885 ABL32267; olek A, RESULT 13 ABL32267 셤 ò g à d à

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                             ATTGATAGTACGTAAGGTTTACATTAGGAGTATCTTGTTGAGCAATCA-TCACTTCG
                                                                                                                          TTACTGTGATGGTCAACTACCCATATGAAATATTTTTTATAAGTCCCATCCTCGAAAGTA
                                                                                                                                                               1014 ATCCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAATTTTCCTTTT
                                                                                                                                                                                 TTGGCGGTATCCATACTGTTAATGAATGTTTTTAATTCATCTGTTTTTGTGAGAAAGATA
          TGTAAAGTGTTCCCTGAATATATAGTACAAAAAGTCATGAGCTTATTCGCTCATGACT
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                                                                                                                                                                                                                                                            ID NO 1931; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                        immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1931.
                                                 TTTTCGTTTAAATGATTTTTTTAAATAAGTTATAAACTTT
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2000DE-01043826
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The present invention provides a number of human immune system associated

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
 the methylation of cytosines. The sequences
genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                            TTATTCGCTCATGACTTTTCGTTTAAATGATTTTTTTTAAATAAGTTATAAACTTTTTA
                                                                                                                                                                                                                                                                     GAACTATCTTCATTTAATTGATAGTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGA
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                                                                                                                                                                                 Gaps
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                                                                                                                     Seguence 14006 BP; 3278 A; 155 C; 3257 G; 7313 T; 0 U; 3 Other;
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                                                                                                                                                                                 Indels
                                                                                                                                                                                 194;
                                                                                                                                                  Score 55.6; DB 6;
Pred. No. 0.038;
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2000DE-01043826.
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nilarity 47.0%;
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                                                                                                                                                       Query Match
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WPI; 2002-147896/19.

XY

Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic PT signal transduction e.g. cancer, comprises chemically modified genomic XX

Claim 1; SEQ ID NO 354; 24pp; English.

XX

Claim 1; SEQ ID NO 354; 24pp; English.

XX

Cramal transduction associated genes. The DNA sequences are chemically condition associated genes. The DNA sequences are chemically condition associated genes. The DNA sequences are chemically condition of bisulphite, hydrogen sulphite or disulphite.

Also disclosed are oligonucleotides and/or PNA oligoners for detecting the cytosine methylation state (CpG islands) of these genes, and a method contained from cells or callular components which contain DNA, e.g. cell contained from cells or callular components which contain DNA, e.g. cell innes, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from embedded in paraffin such as tissue from embedded in paraffin such as tissue from embedded in paraffin such as tissue from exposite combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK11158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence 47108 BP; 15349 A; 429 C; 8736 G; 22594 T; 0 U; 0 Other:
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40870 ACGAATTTAAATTGATTTTTTTTTTTA 40903

Search completed: February 24, 2004, 02:43:29
Job time : 419 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	February 24, 2004, 01:04:17; Search time 3429 Seconds (without alignments) 15446.249 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-019-661-1 1222 1 ctttactgtattgttttatttcatttgggtctctttgagt 1222
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues

6940544

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmbl:* Database :

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em_htgo_mus:* em_htgo_other:* em_sy:* em_htgo_hum:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AF196486 Bacillus	XOEROS Secuencia	50927 B	391415 Sequence	7035 Bacillu	017009 Bacillu	6012	97400 Bacillu	Bacillu	Uncultu	Bacillu	Racillu	AF350930 Bacillus	AX391418 Sequence	AF478056 Bacillus	AY195570 Bacillus	AF478046 Bacillus	AF478048 Bacillus	AF#/0055 BACILIUS	AF4/805/ BACILLUS AF350909 Bacillus	AF478051 Bacillus	AX391417 Sequence	AF478045 Bacillus	AF478050 Bacillus	AF478059 Bacillus	AF350928 Bacillus	1/50		37476 Company	78061	50932	933	090	91420 8	\$21 S	50934 B	78047 B	78049 Bacillu	1422 S	50935 B	780	391423 Sequenc
SUMMERLES	ID	AF196486	AX068093	AF350927	AX391415	AE017035	AE017009	AY460124	AF397400	AF478058	BAC505742	AF350951 AY391419	AF478052	AF350930	AX391418	AF478056	AY195570	AF478046	AF478048	A5470057	AF350929	AF478051	AX391417	AF478045	AF478050	AF478059	AF350928	AIL955/1	A1136412	AX391416	AF478061	35093	33	~	9142	9142	93	04	304	9142	093	7805	9142
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AF196486 1222 bp DNA linear BCT 05-APR-2000 Bacillus sp. 240Bl putative metallohydrolase (aiiA) gene, complete Bacillus sp. 240B1
Bacillus sp. 240B1
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 1222)
Dong, Y.H., Xu, J.L., Li, X.Z. and Zhang, L. H.
AitA, an enzyme that inactivates the acylhomoserine lactone quorum-sensing signal and attenuates the virulence of Erwinia AF196486 AF196486.1 GI:7416988 RESULT 1 AF196486 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

ALIGNMENTS

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CCTGTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAAAATGAAGTGCCA
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Patent: WO 0102578-A 1 11-JAN-2001; Institute of Molecular Agrobiology (SG)
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Sequence 1 from Patent WO0102578.
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                                                            Dong, Y.-H., Xu, J.-L. and Zhang, L.-H.
Dong, Y.-H., Xu, J.-L. and Zhang, L.-H.
Direct Submitssion
Submitted (20-007-1999) Institute of molecular Agrobiology, 1
Research Link, The University of Singapore, Singapore 117604,
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1. 1222
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                          Sci.
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Best Local Similarity 100.0%; Pred. No. 4.7e-213; Matches 1222; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CTTACTGTATTGTTTATTCAAACTAAATGTAAAGGTGGATACATAATGACAGTAAAG 60 1 CTTACTGTATTGTTTATTCAAAACTAAATGTAAAGGTGGATACATAATGACAGTAAAG 60 61 AAGCTTTATTTCGTCCCAGCAGGTGGTTTGTTGGATCATTCGTTAATAGTACA 120 61 AAGCTTTATTTCGTCCCAGCAGTGGTTTGTTGGATCATTCGTTAATAGTACA 120 61 AAGCTTTATTTCGTCCCAGCAGTGGTTGTTGTTGGATCATTCGTTAATAGTACA 120 61 AAGCTTTATTTCGTCCCAGCAGTGGTTGTTGTTGGTGTTATTTGGAGACTGAAGAA 180 121 TTAACACCAGGAGAATTATTAACACCGGTTTACTTTTTGGAGACTGAAGAA 180	TTTT - 	301 AATATTTAAAACGGGTTGGTTATGAGCCGGAAGACCTTCTTTATATTAGTTCTCAC 360	421 CGTGCTGAATATGAGGCGCGCGCGCAGCATAGCGAAGAATTTTGAAAGATGTATATTGCCG 480	CGGT	TTGCGGGATTTGATTCAGAATTAGCTTTAATCTTCAATTAAAGGTTTAAAAGGTGGTGGTGGTGGTGGTGGTGGT	TTCG TTCG	

23-MAR-2002

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Bacillus

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                                                                                                                                                        Zhang, L., Dong, Y.1. and Xu, J.

Bacterial strains, genes and enzymes for control of bacterial
diseases by quenching quorum-sensing signals
diseases by quenching quorum-sensing signals
Patent: WO 0216623-A 2 28-FEB-2002;
Institute of Molecular Agrobiology (SG)
Location/Qualifiers
1. 1339
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llarity 90.6%; Pred. No. 2.5e-179;
Conservative 0; Mismatches 115;
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Sequence 2 from Patent W00216623.
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AX391415.1 GI:19700038
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 1319 CTCATTTGGATCCCTTTGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ankyrin repeat domain protein"
/protein id="AAP27245.1"
/db xref="G1:3025801"
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HIEPTSDFSKLQLKSAIKAESFKKTLNYACMRNDIETVKEKLINIKLSTLNKKGPDRK
TPLHHACLNENIEIVTLLVEAGADLKIKYHGETPFALACRKGNVEIIKYLISQGENAN
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LEMPQSTISQHLSKLKAAKNVTGTRKGLEIYYEVTDNRTKSILACLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Putative prophage; Putative lysogenic prophage region. Best Hits not completed. Putative attL/R; Putative attL occurs within, but close to the terminus of the 3' end of ORF03960, a good house-keeping gene?" 226. 1392
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Submitted (26-MAR-2003) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifican
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/locus_tag="BA3480"
/note="similar to GP:6911992; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="glycosyl transferase, group 2 family
protein/polysaccharide deacetylase family protein"
/protein id="AAP27247.1"
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/protein_id="AAP27246.1"
/db_xref="GI:30258018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Bacillus anthracis phage lambda Ba04"
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/note="similar to GP:1841966; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                             join(1. .259678,310221. .312049)
/organism="Bacillus anthracis str. Ames"
/mol_type="genomic DNA"
/strain="Ames"
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/locus tag="BA3479"
/note="similar to GP:4894353, and
by sequence similarity; putative"
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/db_xref="taxon:229346"
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/locus_tag="BA3479"
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/codon start=1
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I (bases I to 31204)
Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I., Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E., Okstad, O., Helgason, E., Rilstone, J., Wu, M., Kolonay, J., Beanan, M., Dodson, R., Brinkac, L., Gwinn, M., DeBoy, R., Madupu, R., Daugherty, S., Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H., Radmo, J., Bertron, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J., Cline, R., Redmond, C., Thwaite, J., White, O., Salzberg, S., Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
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Nature 423 (6935), 81-86 (2003)
22608414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus anthracis str. Ames section 12 of 18 of the complete
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AE017035/c
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MEDLINE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence similarity; putative" /codon srart-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLYNKAVFSGRGYFKHILTTIFYIALGIGIFRFLFLIYPAWKQKRKTLSRTIHSSYQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALCNSKHKTLGFIALDNMMLFQYVLQFIAPFADILMIIGLFSSDPLKVLGFYFVFFLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="identified by Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 ATACACCAGGCCATACTCCAGGGCATCAATCGCTATTAATTGAGACAGAAAAATCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29097 TACATTTTGATCATGCAGGAGGAACGGTGCTTTTACAAATACACGATTATTGTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29037 GAACGGAATATGAGGCAGCACTTCATAGAGAAGAATATATGAAAGAATGTATATTACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29397 AGCTTTATTTCATCCCAGCAGGTCGTTGTTATGTTAGATCATTCTTCTGTTAATAGTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 ATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGAGTTCAATTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTTTATTTTCGTCCCAGCAGGTCGTTGTATGTTGGATCATTCGTCTGTTAATAGTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAACACCAGGAGAATTATTAGACTTACCGGTTTGGTGTTATCTTTTGGAGACTGAAGAAG
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                                                                                                                                                                                                               /note="similar to GP:6470197; identified by
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                                                                                                                                                                                                                                                                                       terminal protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.5%; Score 1032.2; DB 1;
.larity 90.3%; Pred. No. 7.7e-179;
Conservative 0; Mismatches 118;
                                                                                                                          I FWCYRKDFMAINGFNENMLMAEDADFAKRLKE"
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Matches 1103; Conserv
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131. .1015
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1. .301665
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Bacillus cereus ATCC 14579 section 12 of 18 of the complete genome.
AE017009 AE016877
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Bacillus cereus ATCC 14579
Bacteria; Firmicutes; Bacillales; Bacillus Bacillus
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1 (bases 1 to 301665)

Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candelon, B.,
Kapatral, V., Bhattacharrya, A., Reznik, G., Mikhailova, N.,
Lapidus, A., Chu, L., Mazur, M., Goltsman, E., Larsen, N., D'Souza, M.,
Balunas, T., Grechikin, Y., Pusch, G., Haselkorin, R., Fonstein, M.,
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                                                                                                                                                                                                                                                                                           722 IGAAAGAGAAGCCGAITGIIITCIIIGACAIGAIAIAGAGCAGGAAAGGGGAIGIAAAG
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Candelon, B., Gailloux, K., Ehrlich, D.S. and Sorokin, A.
The number of ribosomal RNA operons in Bacillus cereus
Unpublished
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AUTHORS
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Best Local Similarity
Matches 1092; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MRRFIDTANLEDIKKAYKLGVLAGVTTNPSLVAKEGVKFEDRIA
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HQLDTQITAASVRHPDHVTRVAMGAHTATIPVKVIEGIAMHPLTDGGIEKFAADWAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGAIVAIGIYKANLGKVLLYSLIITFFAAIIAGPĪFAKMIHKRVIPENEPELIRVNTK
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ALSPIVLAFIVAGLIRIATGSATVALTTAAGIVSPIIENTTGVNLELLVIATGAGALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INEXPURYKLYXDOYIDOKISTASATGMPULKSLKWDEBALHVAGITDDKLSKLVPTTHSL
TGLDEBLAKEMUVLVSTPPVVGASDGVLSNLGVNAIDPGVVAVTIGTSGAIRAVTNRP
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                                                                                                                         DSGNHTVVTANYHKGTIESFEVNEENGTVUPDAASIMTHEGSGPNKEROEKPHAHTAGY
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/protein_id="AAP10308_1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (7409. .8077)
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complement (7409. .8077)
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/RC number="2.2.1.2"
/codon start=1
/transl_table=11
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complement (4015. .5556)
/locus tag="BC3369"
/BC_number="2.7.1.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="Transaldolase"
protein id="AAP10311.1"
                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/product="Gluconokinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5687. .7012)
/locus_tag="BC3370"
complement (5687. .7012)
/locus_tag="BC3370"
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/locus tag="BC3372"
/EC_number="1.1.1.44"
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complement (4015. .5556)
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/transl_table=11
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/translation="MQVGLIGLGKMGLNLGKNLMDHKHEVVAPDLNTSAVEEMKEYGA
TGTSSLSEIVQSLQSPRILWYWPHAVVDSYIDBVTPLLSKGDILIBAGNSHYKESIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKAIGLMQYGDKSVLQEIEMQTPLLGDNDVLIEVYAAGVNPVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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/locus tag="BC3375"
/note="similar to Glucose-6-phosphate 1-dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGAGTTCAATTATTGC
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                                                                                                                                        complement(9194. .11187)
/locus_tag="BC3373"
complement(9194. .11187)
/locus_tag="BC3373"
/locus_tag="BC3373"
/note="similar to Transketolase; BC_number 2.2.1.1"
complement(11227. .13474)
/locus_tag="BC3375"
complement(11227. .13474)
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larity 90.0%; Pred. No. 2.1e-176;
Conservative 0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Quinone oxidoreductase"
/protein_id="AAP10313.1"
/db_xref="G1:29897036"
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complement (1.2.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (13851. .14804)
/locus_tag="BC3377"
/BC_number="1.6.5.5"
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                                                                                                                                                                                                                                                                                                                                                                                           EC_number 1.1.1.49"
complement(13851. .1
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GPILVDTGMPESAVNNENLFEGTFAEGGILPKWTEEDRITALKRAGYEPDDLLYIIS SHHFPDHAGGNGAFINYPIIIQRARYEAAQYREATKECILPNLNYKIIEGDFEVVPG VQLLYTPGHSGFGHGGLITEREKSGVVLLTIDASYTKENFEDEVPFAGFDPELALSSIK RLKEVVWKEKPLVFFGHDIEQEKGCKVFPEYI"
                                                                                                                                                                                                                                                                                                     translation="MTVKKLYFVPAGRCMLDHSSVNSTIAPGNLLNLPVWCYLLETEE"
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Direct Submission
Submitted (06-NOV-2003) College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, Hubei 430070, China
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1 (bases 1 to 1369)

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All.-lactonase gene from Bacillus thuringiensis
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/mol_type="genomic DNA"
/strain="CTC"
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/brotein_id="AAM61772.1"

/da xref="id1:21541343"

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SHLHPDHAGGNGAFINVPIITVQRABFRAAQHSEEXLKECILPNLNYKIIEGDYEVVSG
VQLLHTPGHTPGHQGLLIETEKSGSVLLTIDASYTKENFEEEVPFAGFDPBLALSSIK
RLKRVVIKERPIPFFGHDIEQPEKGCKVPPEYI"
                                                                                                                      Score 729; DB 1; L
Pred. No. 4e-123;
0; Mismatches 15;
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Bacillus thuringiensis segene, complete cds.
AF478058
AF478058.1 GI:22095300
                                                                                                                       59.7%;
                                                                                                                                      Similarity 98.0
88; Conservative
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Best Local S:
Matches 738
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      TGAAAGAGAAGCCGCTTGTTTTCTTTGGACATGATATAGAGCAGGAAAAGGGATGTAAAG 988
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(bases 1 to 753)

Reimmann, C., Ginet, N., Michel, L., Keel, C., Michaux, P.,
Krishnapillai, V., Zala, M., Heurlier, K., Triandafillu, K., Harms, H.
Defago, G. and Haas, D.
Genetically programmed autoinducer destruction reduces virulence
gene expression and swarming motility in Pseudomonas aeruginosa
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Reimmann,C., Ginet,N., Michel,L., Keel,C., Michaux,P.,
Krishnapillai,V., Zala,M., Triandafillu,K., Harms,H., Defago,G.
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Biologie, Lausanne, VD 1015,
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/gene="aliA"
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/codon start=1
/transI_table=11
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                                                                                                                                                                                                                                                                                                              ATGGTCAACTACCCATATGAAATATTTTTTATAAGTCCCCATCCTCGAAAGTAATCCACAT
                                                                                                                                         GTACGTAAGGTTTACATCATTAGGAGTATCTTGTTGAGCAATCATCACTTCGTTACTGTG
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                                                                                    TTAAATGATTTTTTAAATAAGTTATAAACTTTTTTAGAACTATCTTCATTTAATTGATA
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                                 TGTTCCCTGAATATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTTCGT
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Batiment de
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/organism="Bacillus sp.
/mol_type="genomic DNA"
/strain="A24"
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1. .753
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AF397400
Bacillus sp. A24 AiiA (aiiA)
AF397400
AF397400.1 GI:21541342
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Submitted (06-JUL-2001)
Universite de Lausanne,
Switzerland
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Bacillus sp. A24
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                                                                        49 ATGACAGTAAAGAAGCTTTATTTCGTCCCAGCAGGTCGTTGTATGTTGGATCATTCGTCT
                                     Gaps
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Length 753;
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TGTATATTGCCGAATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGA
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Appl. Environ. Microbiol. 69 (8), 4989-4993 (2003) 22783888
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/country="United Kingdom:Nottinghamshire"
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Mond type="genomic DNA"
/isolation_source="grassland soil"
/db_xref="taxon:83428"
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AJ505742.1 GI:22293638
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/transl_table=
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Bacillus thuringiensis serovar toumanoffi
Bacillus thuringiensis serovar toumanoffi
Bacieria Frmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 753)
Lee,S.J., Park,S.Y., Lee,J.J., Yum,D.Y., Koo,B.T. and Lee,J.K.
Genes Encoding the N.Acyl Homoserine Lactone-Degrading Enzyme Are
Widespread in Many Subspecies of Bacillus thuringiensis
Appl. Environ. Microbiol. 68 (8), 3919-3924 (2002)
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    .753
    forganism="Bacillus thuringiensis serovar toumanoffi"
/mol_type="genomic DNA"
    fstrain="HD201"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="aiiA"
/note="N-acyl homoserine lactone-degrading enzyme"
                                                                                                                                                                   2 (bases 1 to 753)
Lee,S.-J., Park,S.-Y., Yum,D.-Y. and Lee,J.-K.
Direct Submission
Submitsed (30-JAN-2002) R&D Center, inBioNET Corporation,
Johnin-dong 461-6, Yusong, Deajeon 305-390, Korea
Location/Qualifiers
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Pred. No. 1.5e-115;
0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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/db_xref="GI:22095301"
                                                                                                                                                                                                                                                                                                                                                                                       'note="serovar toumanoffi"
                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:180862"
/clone="16"
                                                                                                                                                                                                                                                                                                                                      serovar="toumanoffi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon start=1
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Best Local Similarity 94.6%;
Matches 712; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                      l. .753
/gene="aiiA"
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                  ORGANISM
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AUTHORS
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BACS05742 753 bp DNA linear BCT 08-AUG-2003
Uncultured Bacillus sp. aii2 gene for N-acylhomoserine lactone
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/db_xref="sPTREMB1:08kNY1"
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GAAAAATCCGGTCCTGTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAA
                                                                                                                                                                                                                                                         541 GAGAACTCTGGTCCAGTGTTATTAACAATCGATGCATCGTATACAAAAGAAAATTTTGAA
                                                                                                                                                                                                                                                                                                                                649 AATGAAGTGCCATTTGCGGGATTTGATTCAGAATTAGCTTTATCTTCAATTAAACGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 AAAGAAGTIGIGATAAAAGAGAAGCCAATIGITTTICTTIGGGCATGATATAGAGCAGGAA
                                                                                GTTCAATTATTGCATACACCAGGCCATACTCCAGGGCATCAATCGCTATTAATTGAGACA
                                                                                                                                                                                                                                                                                                                                                                                         601 GATGAAGTGCCATTTGCGCGATTTGATCCAGAATTAGCTTTATCTTCAATTAAACGTTTA
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The Ti Plasmid of Agrobacterium tumefaciens Harbors an attM-Paralogous Gene, ailB, Also Encoding N-Acyl Homoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ail2 gene; N-acylhomoserine lactone lactonase.
uncultured Bacillus sp.
uncultured Bacillus sp.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
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SHLHYPGHSGRGARGAFLLIFEKSGPVLLTIDASYTKENFEDEVPFAGFDSELALSSIK
RIKEVVMKEKPIVFFGHDIEQEKGCKVFPEYI"
                                                                                                                                   National University of Singapore, 1 Research Link, Singapore 117604 Location/Qualifiers
           Dong, Y.H., Gusti, A.R., Zhang, Q., Xu, J.L. and Zhang, L.H. Identification of quorum-quenching N-acyl homoserine lactonases from Bacillus species Appl. Environ. Microbiol. 68 (4), 1754-1759 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCATTATACAACGTGCTGAATATGAGGCAGCGCGGCATAGAGAGGAATATTTGAAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 753;
                                                                                                                                                                                                                                                                                                           /gene="aiiA-B18"
|note=N-acyl homoserine lactone hydrolase"
|codon start=1
|transl_table=11
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                                                                                                                        and Zhang, L.H.
                                                                                                                                                                                               1. .753
/organism="Bacillus thuringiensis"
/mol type="genomic DNA"
/strain="B18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 644.2; DB 1;
Pred. No. 1.2e-107;
0; Mismatches 68;
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                                                                                                            2 (bases 1 to 753)
Dongy,Y.H., Gusti,A.A., Xu,J.L. and
Direct Submission
Submitted (21-FEB-2001) Institute
                                                                                                                                                                                                                                                                                /gene="aiiA-B18"
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91.0%;
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SHLHPDHAGGNGAFTNTPIIVQRAEYEAAQHSEEYMKECILPNLKYKIIEGDYEVPG
VQLLYTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFEDEVPFAGFDSELALSSIK
RLKEVVRKENPIVFFGHDIEQEKSCKVFPEYI"
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Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacilus
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753 bp DNA linear BCT 05-AUG-2002
Bacillus thuringiensis serovar kyushuensis AliA-like protein (aliA)
AP478052
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GPILVDTGMPESAVNNENLFDGTFVEGQILPKMTEEDRIVNILKRVGYEPEDLLYIIS
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Bacillus thuringiensis serovar kyushuensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus, Bacillus
                        361 ATCATTATACAACGTGCTGAATATGAGGCAGCAGCAGCATGAGAGGAATATTTGAAAGAG
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Lee,S.J., Park,S.Y., Lee,J.J., Yum,D.Y., Koo,B.T. and Lee,J.K.
Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Japespread in Many Subspecies of Bacillus thuringiensis
Appl. Environ. Microbiol. 68 (8), 3919-3924 (2002)
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/transI table=11
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Lee,S.-J., Park,S.-Y., Yum,D.-Y. and Lee,J.-K.
Lee,S.Jumission
Direct Submission
Submitted Gudal-ANA-2002) R&D Center, inBioNET Corporation,
Jonmin-dong 461-6, Yusong, Deajeon 305-390, Korea
Location/Qualifiers
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/protein_id="AAM92133.1"
/db_xref="GI:22095289"
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/strain="HD541"
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/clone="9"
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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Bacterial strains, genes and enzymes for control diseases by quenching quorum-sensing signals batent: WO 0216623-A 6 28-FEB-2002; Institute of Molecular Agrobiology (SG) Location/Qualifiers
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Corganism="Bacillus thuringiensis"
/mol type="unassigned DNA"
/db_xref="taxon:1428"
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Sequence 6 from Patent WO0216623
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                                                                                                                                                                                                of Molecular Agrobiology, The
1 Research Link, Singapore 117604
1 (bases 1 to 753)

Dong, Y.H., Gusti, A.R., Zhang, Q., Xu, J.L. and Zhang, L.H.

Identification of quorum-quenching N-acyl homoserine lactonases

from Bacillus species

Appl. Environ. Microbiol. 68 (4), 1754-1759 (2002)
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                                                                                                                                                          and Zhang, L.H.
                                                                                                                                                                                                                                                               1.753
Corganism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/strain="B17"
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Pred. No. 9.9e-106;
0; Mismatches 74;
                                                                                                                                     Dong, Y.H., Gusti, A.A., Xu, J.L. and Direct Submission Submitted (21-FEB-2001) Institute National University of Singapore, Location/Qualifiers
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Best Local Similarity 90.2%;
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  SHLHFDHAGGNGTFTNTPILVQRAEVETAQHSEEYLKECILPNLNYKIIBGDYEVVPG
VQLLYTPGHTPGHQSLPIETENSGPVLLTIDASYTKENFEDEVPFAGVDSELALSSIK
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Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus, Gacillus
cereus group.
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                                                                                                    ore 634.2; DB 1;
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Mismatches 74;
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                                                                                                                                                                        GAAAAATCCGGTCCTGTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAA
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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   GTTCAATTATTGTATACGCCAGGTCATTCTCCAGGCCATCAGTCGCTATTAATTGAGACA
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                                                             AAAGAAGTGGTGATGAAAGAGAAGCCGATTGTTTTCTTTTGGACATGATATAGAGCAGGAA
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                                GAAAAATCCGGTCCTGTATTAATAACGATTGATGCATCGTATACGAAAGAGAATTTTGAA
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Bacterial strains, genes and enzymes for control of bacterial diseases by quenching quorum-sensing signals
Patent: WO 0216623-A 5 28-FEB-2002;
Institute of Molecular Agrobiology (SG)
Location/Qualifiers
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    .753
/organism="Bacillus thuringiensis"
/mol_type="unassigned DNA"
/db xref="taxon:1428"
/note="B17"

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Pred. No. 9.9e-106;
0; Mismatches 74;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 20, 2004, 16:19:22; Search time 17 Seconds (without alignments) 691.569 Million cell updates/sec

US-10-019-661-2 1315

1 MIVKKLYFVPAGRCMLDHSS.....VFFGHDIBQERGCKVFPEYI 250 Title: Perfect score: Sequence:

127863 seqs, 47026705 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	OSOGES mycobacteri	057744 methanococc		3 aquifex a	methanoc		~	Q57544 haemophilus	P52700 xanthomonas		P54501 bacillus su		P53965 saccharomyc	-		emericell		P00890 saccharomyc		~		_	_		~	_	5 buchnera	3 aeromonas	6	80	33	۸,	-
SUMMARIES	ID	YNOO MYCTU	Y296 METUA	YFLN BACSU	YL35_AQUAE	Y047 METUA	GL2M_ARATH	Y888 METJA	YCBL_HAEIN	BLA1_XANMA	GLO2_YEAST			YND2 YEAST	GL2C ARATH	YYBB BACSU	CISY_EMENI	GIDA_CHLMU	CISY_YEAST	YOUP BACSU	Y274 METUA	CISY_ASPNG	GLO2_BUCAP	YL54_CAEEL	GLO2_HUMAN	SM2A_DROME	PKSL_BACSU	GLO2_BUCAI	BLAB_AERHY	Y301 METJA	FNBA STAAU	GLO2_CALJA	DGT1_RICPR	Y162_METJA
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Y861 METJA Y448 METJA GLO4 YEAST BUD2 YEAST ITA2 HUMAN CARA PYRFU CRAA PYRFU CRAA PYRFU FPRA METTM ENO STAEP TL40 SPIOL YXT2 CAEEL MCK XENLA GYRB TREPA
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Serlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterback T.K., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                           39 LLETEEGPILVDIGM-----PESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVG
                                                                                                                                                                                                                              GVOLLHTPGHTPGHQSLLIETEKSGPVL
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                                                                Gaps
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                                Length 310;
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Pfam; PR00753; lactamase B; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 203 AA; 23236 MW; 9039A9CB6DF9E75D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales;
0764F4FA64AB5E51 CRC64;
                                                                87;
                                 11.9%; Score 157; DB 1; 25.7%; Pred. No. 4.9e-06; ive 34; Mismatches 87
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01-NOV-1997 (Rel. 35, Last sequence update)
Hypothetical (Rel. 40, Last annotation update)
MJ0296.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A. 2661 / ATCC 43067;
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   34352 MW;
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                                                                   Conservative
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     310 AA;
                                                    Local Similarity
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RA KUNST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA KUNST F., Ogasawara N., Moszer I., Albertini A.M., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Bourstier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Broil S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Fune S., Gallach S.D., Emmerson P.T.,

RA Britz C., Fujita M., Fujita Y., Fune S., Gallaci B., Gallacon N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,

RA Joris B. Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B. Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B. Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Medina N., Meotter P., Koningstein G., Krogh S., Kumao M.,

RA Medina N., Mellado R.P., Mizumo M., Moestl D., Nakai S., Noback M.,

RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Steveni M., Tarconi E., Takagi T., Takamaru P., Jakemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Takemaru A.,

RA Tosarco V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
                                                                                                                                                                         99 YIISSHIHFDHAGGNGAFINTPIIVQRAEYEAAQHSEEYLKECILPNLNYKIIEGDYEVV 158
                                                                                                                                                                                                                                                                                       127 --IBIIETPGHTYGSISVIXK----DYVVVGDASPLKNNILKMIPPKLNVDEKLALESL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
                                                                                                                                                                                                       LS9 PGVQLIHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENEV-PFAGFDSELALSSI
                                                                                    LLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLL
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                                             26;
DB 1; Length 203;
                                             Indels
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                                                  63;
                         7.4e-06;
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Last annotation update)
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  ; Score 152; DB
; Pred. No. 7.4e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                            218 KRLKE------VVMKEK 228
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                                                                                                                                    44 LIITDNNNIIVDTSTKDM-----
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MEDLINE=97417488; PubMed=9272861;
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         11.6%;
24.3%;
      Query Match
Best Local Similarity 24.33
Matches 49; Conservative
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
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Tue Feb 24 12:13:12 2004

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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITRE=20465561; PubMed=11029430;
Warner J.B., Krom B.P., Magni C., Konings W.N., Lolkema J.S.;
Warner J.B., Krom B.P., Magni C., Konings W.N., Lolkema J.S.;
Warner J.B., Strong and induction of the Mg(2+)-citrate transporter CitM of Bacillus subthis."
J. Bacteriol. 182:6099-6105 (2000).
-!-INDUCTION: Expression is under strict control of the medium composition. Induced by citrate, probably via the two-component regulatory system citT/citS. Repressed by rapidly metabolized carbon sources like glucose, glycencol and inositol, via the carbon catabolite repression system. Is also repressed by succinate and glutamate, albeit to a lesser extent.
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshida K., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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                                                                                                                                                                                                                                             Yamamoto H., Murata M., Sekiguchi J.;
"The CitST two-component system regulates the expression of the
Mg-citrate transporter in Bacillus subtilis.";
Mol. Microbiol. 37:898-912(2000).
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EMBL; Z99108; CAB12591.1; -.
PIK, D69811, D69811.
Subtilist; BG12949; yflN.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
                                                                                                                                                                                                                  MEDLINE=20430113; PubMed=10972810;
                                                                                                                                                                     TRANSCRIPTIONAL REGULATION.
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                                                                                                                  Nature 390:249-256(1997).
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211 AA.

PRT;

STANDARD;

RESULT 4 YL35_AQUAE ID YL35_AQUAE

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| RVGDVEFKVLHTPGHTPG---LCCLYEEKRRVLIAGDLLFKGSVGRWDLPGGN-----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Hydrolase; Zinc; Complete proteome.
54 ZINC 1 (BY SIMILARITY).
56 ZINC 1 (BY SIMILARITY).
59 ZINC 2 (BY SIMILARITY).
59 ZINC 2 (BY SIMILARITY).
129 ZINC 1 (BY SIMILARITY).
148 ZINC 1 AND 2 (BY SIMILARITY).
148 ZINC 1 AND 2 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
-!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
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  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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HSSP; Q16775; 1QHS.
InterPro; IPR001279; Blactmase-like.
Pfam: PF00753; lactamase_B; l.
                                                                                                                                                                                                                                                                  STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
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22958 MW;
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                                                                                                                                                                                  NCBI_TaxID=63363;
                                                                                                           AQ_2135.
Aquifex aeolicus.
30-MAY-2000
30-MAY-2000
16-OCT-2001
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15-DEC-1998
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GLX2-1 OR AT2G43430 OR T1024.17.
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  88 THE TETTETTETTER BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREEF BREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 GELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNIL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GL2M_ARATH
GL2M_ARATH
GL2M_ARATH
STANDARD; PRT; 331 AA.

AC 024495; 022857; 024494;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DF 49-FEB-2003 (Rel. 41, Last annotation update)
DF 49-FEB-2003 (Rel. 41, Last annotation update)
DF Glyoxalase II) (Glx II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AEYEAAQHSEEYLKECI---LP-NLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIETE
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                                                                                                                                                                                                                   MEDIINE=96337999; PubMed=8680887;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
-!- SIMILARITY: STRONG TO M.JANNASCHII MJ0162 AND MJ1236. ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 115.5; DB 1; Length 428; 20.8%; Pred. No. 0.025; Ive 44; Mismatches 73; Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: IPR001279; Blactmase-like.
Pfam; PP00753; lactamase B; 1.
Hypothetical protein; Complete proteome.
SRQUENCE 428 AA; 48492 MW; A649ED66705AA01B CRC64;
                                                                      Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 KRVGYEPEDLLYIISSHLHFDHAGGNGAF----INTPII---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILAR TO SYNECHOCYSTIS PCC 6803 SLL0514.
                                                                                                                                                                      FROM N.A.
AI.-1 / DSM 2661 / ATCC 43067;
     Hypothetical protein MJ0047. MJ0047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67462; AAB98027.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Conservative
                                                       Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 51; Conserv
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                                                                                                                           NCBI TaxID=2190;
                                                                                                                                                                                                         STRAIN=JAL-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis B.W., Ecker J.R., Theologis A.;
Strain Arabidopais full length cDNA clones (RAFLs) sequenced by the Shinozaki W. Salk/Stanford/PoBSC)."
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databases.
LACTOYL-GLUTATHIONE TO FORM GUITATHIONE AND D-LACTIC ACID.
C.-I- CATALYTIC ACTIVITY: (S)- (2-hydroxyacyl)glutathione + H(2)O = glutathione + a 2-hydroxy acid anion.
C.-I- CATALYTIC ACTIVITY: (S)- (2-hydroxyacyl)glutathione + H(2)O = clopacy acid anion.
C.-I- PATHWAY: Glyoxal pathway.
C.-I- PATHWAY: Glyoxal pathway.
C.-I- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surematophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. Columbia;

STRAIN=CV. Columbia;

MEDLINE=20083487; PubMed=10617197;

MEDLINE=20083487; PubMed=10617197;

MEDLINE=20083487; PubMed=106.71., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Romning C.M., Koo H.L.,

Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001279; Blactmase-like.

Pfam; PF00753; lactamase_B; 1.

Hydrolase; Zinc; Mitochondrion; Transit peptide.

TRANSIT 1 76

HYDROXYACYLGLUTATHIONE HYDROLASE.

TRANSIN 77 331

HYDROXYACYLGLUTATHIONE HYDROLASE.
                                                                                                                                                                                                                                                                   STRAIN=cv. Wassilewskija;
MEDINES9009981; Pubmed=9349270;
MaitinEs9009981; Krishnasamy S., Owen H.A., Makaroff C.A.;
"Molecular characterization of glyoxalase II from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
D -> H (IN REF. 1; AAC49866).
W, ZEDC2184902419C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 35:471-481(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC002335; AAB64315.2; -- EMBL; AX091277.1; -- EMBL; AX091278; AAM14217.1; -- EMBL; AY063806; AAL36162.1; -- HSSP; Q16775; 1QHS.
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=3702;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                -----TVGVVDP--SEAAPVIEALSRKNW---NLTYILNTHHHDDHIGGN----- 140
                                                                                                                                                                                                                                                                                   60 NEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------AELKERYGAKVIGSAVDKDRIPGIDILLKDSDKWMFAGHEVRILDTPGH 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 TPGHQSLLI---ETEKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMK 226
                                                                                                                                             2 TVKKLYFVPAGRCMLDH--SSVNSTLTPGELLDLPVWCYLLETREGPILVDTGMPESAVN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                     120 PIIVQRAEYEAAQHSEEYLKECI------LPNLNYKIIEGDYEVVPG--VQLLHTPGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96337999; DubMed=8688087;
MEDLINE=96337999; DubMed=8688087;
MEDLINE=96337999; DubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
-!- SIMILARIȚY: WEAK, TO B.SUBTILIS YQGX AND TO M.JANNASCHII MJ0296.
                                                                                                                                                                                                                62 TLKITHF-----CSISNMPSSLKIELVP---CSKDNYAYLLHDE-----DTG---
                                                                                  18.
           DB 1; Length 331;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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Pfam; PF00753; lactamase B; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 206 AA; 23229 MW; AC2C59FFIE80840E CRC64;
       8.7%; Score 114.5; DB 1;
22.8%; Pred. No. 0.022;
ive 38; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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or send an email to license@isb-sib.ch).
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                                                                          57; Conservative
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Q58298;
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Matches 57
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Length 206;

8.6%; Score 113; DB 1; 24.1%; Pred. No. 0.015;

Query Match Best Local Similarity

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                                     106
                                                                                               107 FDHAGGN----GAFINTPIIVQRAEYEAAQHSEEYLKECILPNLNYKIIEGDYEVVP---- 159
                                                                                                                  58 FDHTSADYLIEEYFNCPTIIEDKEVKHLKNGD----EVTVSSLFGAKLNPPKEIIPLSEI 113
                                47 ILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLH
                                                        -!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY. STRONG, TO E.COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95350630; PubMed=7542800;
Richamn R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Reischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom B. Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
     48;
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 112.5; DB 1; Length 212; Pred. No. 0.018;
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ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
A09D4E7DA445F4AA CRC64;
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                                                                                                                                                                 -----GVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASY 194
     45;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase, Zinc;
                                                               23 İLIDPGT-----SGTF----
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HI1663.
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39; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
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151
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METAL 55 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter J.C.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                               HOSLLIETEKSGPVLLTIDASYTKENFENEVPFAG------FDSELALSSIKRLKEV 223
                                                                                                                          -----KVAFTGDVLFQGGIGRTDFPRGDYETLISSI-RIKLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-XAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=99030465; PubMed=9811546;
Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S.,
Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S.,
Ullah J.H., Malsh T.R., Taylor I.A., Emery D.C., Verma C.S.,
Ullah J.H., Spencer J.;
The crystal structure of the L1 metallo-beta-lactamase from
Stenotrophomonas maltophilia at 1.7 A resolution.";
J. Mol. Biol. 284:125-136(1998).
-!- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMIPENEM. UNSTABLE BELOW PH
8, UNLESS ZINC IS PRESENT.
-!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
                       79 EEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTPIIVQRAEYEAAQH----
                                              -----AAMQLKQHFGVEI
                                                                 134 ----SEEYLKECI-----LPNLNYKI-----IEGDYEVVPG--VQLLHTPGHTPG
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=IID 1275;
MEDLINE=94289479; PubMed=8018721;
Walsh T.R., Hall L., Assinder S.J., Nichols W.W., Cartwright S.J.,
Macgowan A.P., Bennett P.M.;
"Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas
  71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bicknell R., Emanuel B.L., Gagnon J., Waley S.G.; "The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275."; Biochem. J. 229:791-797(1985).
                                                                                                                                                                                                                                                                                      Metallo-beta-lactamase L1 precursor (Beta-lactamase, type II) (EC 3.5.2.6) (Penicillinase). Xanthomonas maltophilia (Pseudomonas maltophilia (Stenotrophomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid.
-!- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
-!- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced
enzymatic activity in presence of Co(2+), Ni(2+), Cd(2+), and
                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to the class-B beta-lactamase family.
   56; Indels
                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                     290 AA.
   Mismatches
                                       Biochim. Biophys. Acta 1218:199-201(1994).
                                                                                                                                                         224 VMKEKPIVFFGH----DIEQERGCKVF 246
                                                                                                                                                                          : : |: || ||: |
181 PLNDDIIIIAGHGSYTTIGQEKRSNPF 207
                                                                                                                                                                                                                                                                                                                                                   Xanthomonadaceae; Stenotrophomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=IID 1275;
MEDLINE=86025393; PubMed=3931629;
     Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                      HIG-FIEHEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 34-65.
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                                                                                                                                                                                                                                                                                                                              maltophilia).
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     51;
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                                                                               PRGMI, PF00733; lactamase B; 1.
PROSITE; PS00743; BETA_LACTAWASE B 1; 1.
PROSITE; PS00744; BETA_LACTAWASE B=2; FALSE_NEG.
Hydrolars; Zinc; Antibiotic resistance; Periplasmic; Signal;
Mydrolare.
                                                                                                                                     METALLO-BETA-LACTAMASE L1
                                                                                                                                                                                                    AS -> QR (IN REF. 2).
Q -> A (IN REF. 2).
TED -> RQH (IN REF. 2).
L -> H (IN REF. 2).
                                                                                                                       POTENTIAL
                                                       PDB; 1SML; 20-SEP-99.
Interpro; IPR001018; Beta_lactamase_B.
Interpro; IPR001279; Blactmase-like.
                                                                                                                                                    ZINC 1.
ZINC 1.
ZINC 2.
ZINC 1.
ZINC 2.
                                         EMBL; X75074; CAA52968.1; -.
                                                                                                                        139
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163
168
170
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194
196
203
211
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113
120
127
136
                                                  PIR; S45349; S45349
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146
1147
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1171
1183
1195
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                                                                                                                                                                                                                                                                                                                                                        99 YIISSHLHFDHAGGNGAFINTPI--IVQRAEYEAAQHSEEYLKECIL------ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PNLNYKIIEGDYEVVPGVQLL--HTPGHTPGHQS-LLIETEKSGPVLLTIDASY 194
                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                        ----SHLLDNMKARGVTPRDLR
                                                                                                                                                                                                                                                  39 LLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bito A., Haider M., Hadler I., Breitenbach M.; "Identification and phenotypic analysis of two glyoxalase II encoding genes from Saccharomyces cerevisiae, GLO2 and GLO4, and intracellular localization of the corresponding proteins."; J. Biol. Chem. 272:21509-21519(1997).
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hydroxyacylglutathione hydrolase, cytoplasmic isozyme (EC 3.1.2.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                 59;
                                                                                                                                              Length 290;
                                                                                                                                                                                              57; Indels
                                                                               290 AA; 30801 MW; 0B34CAB54518BC1E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutathione + a 2-hydroxy acid anion.
                                                                                                                                        DB 1;
                                                                                                                                        Score 110.5; DB Pred. No. 0.039;
                                                                                                                                                         21.5%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Glyoxalase II) (Glx II).
GLO2 OR YDR272W OR D9954.5.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic.
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                                                                                                                                     8.4%;
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63 LVQTPDGAVLLDGGMPQMA-
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                                                                                                                                                                                            40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                  Similarity
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STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
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MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
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NCBI_TaxID=1423;
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28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yqgX.
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SEQUENCE FROM N.A.
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Entiator F., Devine W.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entiator F., Devine M.M., Pujita Y., Fabret C., Ferrari E., Foulger D., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Fritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N., Ghiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Karamata D., Kasahara Y., Klaerr.-Blanchard M., Klein C., Robayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Karita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Redigua N., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Rescon B., Nogaa K., Ogiwara A., Oudega B., Park S.H., Rarro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Rapoport G., Rey M., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekleychi A., Tacconi E., Takadishi H., Takemaru K., Festovhi A., Tacconi E., Takadishi H., Takemaru K., Vastuchi M., Tamakoshi A., Tarahashi H., Takemaru K., Vastuch M., Wambut R., Wambut R., Wedler E., Wedler E., Wedler E., Vastuct R., Wedler E., Weller E., Wedler E., Weitzen E., Yoshikawa H., Danchin A., Tarameton P., Wamanc K., Yasumoto K., Yata K., Wamiters P., Wipat A., Tamamoto H., Yamane K., Yasumoto K., Yata K., Wamiters P., Wipat A., Tamamoto G. the Gram-positive bacterium Bacillus R., Ruhlishi H., R., Ruhlishi H., R., Ruhlishi H., R., Ruhlishi H., R., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhlishi H., Ruhli
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-!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
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EMBL; Z99116; CAB14410.1; -.
PTR; A69958; A69958.
Subtilist; BG11691; yggx.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
Hypothetical protein; Hydrolase; Zinc;
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makhino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
Or Sepponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3137-155(1996).
                                                                                                                                                                                                                                                                                                                   MEDLINE=97426617; PubMed=9278503; Blatther F.K., Punkett G. III, Bloch C.A., Perna N.T., Burland V., Baltther F.K., Plunkett G. III, Bloch C.A., Rode C.K., Maybew G.F., Gregor J., Collado-Vide U., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; Sequence of Escherichia coli K-12."; science 277:1453-1474(1997).
                                                                                                                                                                                                            Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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1- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY. STRONG,
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                                                                                               215 AA
                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
WPOCHPICAL protein ycbL.
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BcoGene; EG13704; ycbL.
InterPro; IPR001279; Blactmase-like.
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Hypothetical protein; Hydrolase;
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| : | | | : 182 EHTLVLSGHGPETD 195
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Matches 53; Conserv
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                                                                                                                           67 ELAQHYGVPVFGPEKEDEFWLQGLPAQSRMFGLEECQPLTPDRWLN----EGDTISIGNV 122
                                                                                                                                                                      --QLLHTPGHTPGHQSLLIETEK---SGPVLLTIDASYTKENFENEVPFAGF---DSELA 213
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EEDRIVNIL-----KRVGYEPED----LLYIISSHLHFDHAGGNGAFINTPIIVQRAEY 128
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                                                                                      ---LKEC--ILPN--LNYKIIEGDYEVVPGV 161
                                                                                                                                                                                                                 -----FKGGVGRSDFPRGDHNQL 171
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01-0CT-1996 (Rel. 34, last annotation update)
Hypothetical 32.8 kDa protein in NCE3-HHT2 intergenic region.
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                         Indels
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Hilbert H., Moestl D.,
Submitted (MAX-1996) to the EMBL/GenBank/DDBJ databases.
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20.2%; Pred. No. 0.1;
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                                                                                                                                                                                                                                                          LSSIKRLKEVVMKEKPIVFFGH
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01-OCT-1996 (Rel. 34, Last seq
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SGD; S0004977; SIW14
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                                                                                  129 EAAQH---
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RELINEZ-21016720; bubMed=11130713;

RELINEZ-21016720; bubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B., Balanoubat M., Boutry M., Grivell L.A., Mache R., buigdomenech P., Robert C., Brichelt D., Stantone V., Choisne N., Artiguenave F., Robert C., Burottier P., Robert C., Bencet P., Robert C., Bencet P., Robert C., Perobs M., Bense V., Robert M., Mueller-Auer S., Gabel C., Fuchs M., Bense V., Robert M., Perez-Perez B., Gremath P., Nordsiek G., R., Wurmbach E.; Drzonek H., Perez-Perez A., Teucha P., Nordsiek G., Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Razon M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta B., Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., Marstro P., Stlore M., Miltscher J., Schorf R., Town C.D., Koo H.L., Tallon L.J., Jenkins J., Roborey T., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J. R. Raser C.M., Kalls R., Wu D., Salzberg S.L., White O., Venter J. R. Raser C.M., Kaneko T., Nierman W.C., Salzberg S.L., White O., Venter J. C., Rasencto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Raser C., Kohara M., Salzberg S.L., White O., Venter J. K., Kayasma S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., Nakaawa S., N
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydroxyacylglutathione hydrolase cytoplasmic (EC 3.1.2.6) (Glyoxalase
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-!- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oinchistration bubbed-3349270;
Maiti M.K., Krishnasamy S., Owen H.A., Makaroff C.A.;
Molecular characterization of glyoxalase II from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and characterization of the thiolesterase glyoxalase II from Arabidopsis thaliana.";
Biochem. J. 322:449-454(1997).
                                                                                                                                                                                                                                                                                                                                                          024496; 004844;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                             258 AA.
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STRAIN-cv. Columbia; TISSUB-Leaf;
MEDLINE-97218101; PubMed-9065762;
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244 -----KVFPEY 249
                                                                                       232 QNWSLTMIFDEY 243
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    93 EPEDLL-----YIISSHLHFDHAGGNGAFINTPIIVQRAEYEAAQHSEEYLKEC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VQLLHTPGHTPGHQSLLIE-TEK 182
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Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus
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ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
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ZINC 1 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                      6703B98A8F902B5A CRC64;
glutathione + a 2-hydroxy acid anion.
-!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
-!- PATHWAY: Glyoxal pathway.
-!- SUBCELLULAR LOCATION: CYCOPIASMIC.
-!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                51;
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(Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)
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33; Mismatches
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EMBL; Y08357; CAA69644.1; -.
EMBL; AC011708; AAF19564.1; -.
HSSP; 06775; 1QH5.
InterPro; IPR001279; Blactmase-like.
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                                                                                                                                                                                                          Pfam; PF00753; lactamase_B; 1. Hydrolase; Zinc.
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28-FEB-2003
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P37502;
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Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

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R. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

R. Persecan E., Pujic P., Purnelle B., Ropewollik S., Persectt A.M.,

R. Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

R. Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

A Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

R. A Takeuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K.,

A Tosato Y., Wandeler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler 
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cilis chromosome containing the replication origin."; Res. 1:1-14(1994).
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PIR, S65995; S65995.
Subritist, BG10029; yybB.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase B; 1.
Hypothetical protein; Complete proteome.
SRQUBNCE Z2 AA; Z5266 MW; 57AF02520BA1A3C5 CRC64;
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9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 9011, Ap Sequence 13378, A Sequence 2716, Ap Sequence 1704, Ap Sequence 1669, Ap Sequence 8, Appli Sequence 8756, Ap Sequence 9011, Ap Appli Appli Appli Appli Appli Sequence 8, Sequence 8, Sequence 8 Sequence 8 Description Sequence Sequence 5 US-10-156-761-8756 5 US-10-156-761-9011 2 US-10-156-761-13378 2 US-10-264-237-2716 5 US-10-264-237-2716 5 US-10-156-761-7704 1 US-09-925-301-1224 2 US-10-216-1669 2 US-10-216-1669 2 US-10-219-066-8 2 US-10-219-066-8 2 US-10-219-068-8 2 US-10-219-068-8 2 US-10-219-068-8 2 US-10-219-068-8 2 US-10-219-068-8 2 US-10-219-068-8 2 US-10-219-068-8 Query Match Length DB 361 361 361 Score 142.5 130.5 123.5 120.5 119 109.5 109 109 109 109 109 Result Š.

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US-10-219-475-8	US-10-219-480-B	US-10-219-483-8	US-10-219-525-8	US-10-219-526-8	10-219-	US-10-219-531-8	US-10-219-532-8	US-10-219-533-8	US-10-230-437-8	US-10-232-228-8	US-10-232-226-8	_	US-10-227-884-8	US-10-230-163-8	US-10-230-338-8	US-10-218-631-8		US-10-216-159A-8	US-10-218-849-8	US-10-227-873-8	US-10-227-883-8	US-10-219-076-8	-10-230-	US-10-219-003-8	US-10-219-075-8	US-10-219-464-8	US-10-219-466-8	US-10-219-479-8	US-10-219-481-8
12	12	12	12	12	12	12	12	12	12	12	12	12	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361
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109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109	109
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

145 95 96 DLLYIISSHLHFDHAGGNGAFINTPIIVQRAEYEAAQ-----HSEEYLKE-----CILPN 37 CYLLETE-EGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPE cn 11.7%; Score 153.5; DB 15; Length 290; 1 Similarity 25.7%; Pred. No. 2.5e-07; 61; Conservative 44; Mismatcher APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRERENC: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109 Sequence 8756, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION: ; OKGANISM: Streptomyces avermitilis US-10-156-761-8756 Query Match Best Local Similarity US-10-156-761-8756 TYPE: PRT ORGANISM: Best Loca Matches g à d

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HS-----BEYLKECILPNLNYKIIEGD-YEVVPGVQLLHTPGHTPGHQSLLIETEKSGP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----INTPIIVQRAE-----YEAAQ 132
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146 -LNYKIIEGD----YEVVP-----GVQLLHTP--GHTPGHQSLLIETEKSGPVLLTI-DA 192
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                                                                                                              -----IVOALTGIGRRP
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                                                                                     -FAGFDSELALSSIKRLKEVVMK--EKPIVFFGHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;; Score 142.5; DB 15;
; Pred. No. 2.7e-06;
31; Mismatches 75;
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PRICR APPLICATION NUMBER: JP 2001-204089;

PRICR FILING DATE: 2001-05-30

PRICR APPLICATION NUMBER: JP 2001-272697;

PRICR APPLICATION NUMBER: JP 2001-272697;

PRICR PILING DATE: 2001-08-02;

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 9011

LENGTH: 249

TYDE- NAME OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                 Sequence 9011, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: BHIKAWA, HIROSHI
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRA, HYOSHIYUKI
APPLICANT: SHIRA, TADAXYOSHI
APPLICANT: MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13378, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces avermitilis US-10-156-761-9011
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Best Local Similarity 25.4%
Matches 59; Conservative
                                                                                        193 SYTKENFENEVP
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US-10-156-761-13378
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-10-156-761-9011
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APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

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; LOCATION: (250); corner in the twenty naturally occurring L-amino acids US-10-264-237-2716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 YEVVPGVQLLHTPGHTPGHQ---SLLIETEKSGPVLLTIDASYTKENFENEVPFAGFDSE 211
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                                                                                                                                                                                                                                                                                                                                 38 YLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDL 97
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                                                                                                                                                                                                                                                        Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPRENCE: PA13191 CURRENT APPLICATION NUMBER: US/10/264,237 CURRENT FILING DATE: 2002-10-04 PRIOR APPLICATION NUMBER: PCT/US01/16450 PRIOR FILING DATE: 2001-05-18 PRIOR FILING DATE: 2001-05-18 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 SOFTWARE: PAECHING DATE: 2000-05-19 SOFTWARE: PAECHING DATE: 2010-05-18 SOFTWARE: PAECHIN Ver. 3.1 SEQ ID NO 2716
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25.4%; Pred. No. 0.00031;
iive 28; Mismatches 71
                                                                                                                                                                                                                                                        Score 130.5; DB 1:
Pred. No. 8.6e-05;
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                                                                                                                                                                                                                                                                                               29; Mismatches
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILLING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13378
LENGTH: 372
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Publication No. US20040009491A1
GENERAL INFORMATION:
                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13378
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Best Local Similarity
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Matches 60; Conserv
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; Sequence 1669, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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les 50; Conserv
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US-10-369-493-1669
                                                          NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GGNGAFINTPIIVQRAEYEAAQHSEE-----YLKECI--LPNLNYKIIEGDYEVVPGVQL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 LHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEV 223
---FERS---GDEDSW 207
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                                                                 212 LALS-----SIKRL---KEVVM-----KEKPIVFFGHDIEQERG-CKVF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.2%; Score 120.5; DB 15; Length 378;
Best Local Similarity 22.2%; Pred. No. 0.00096;
Matches 43; Conservative 34; Mismatches 74; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1224, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; TITLE OF INFORMATION:
; TITLE OF INFORMATION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR PILING DATE: 2000-03-08
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SEQ ID NO 1224
; LENGTH: 298
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159 LQLGPGLEVWATPGH--GGQRDVSVVVAGTALGTVVVAGDV-
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: ISHIKAWA, UUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7704
                                                                                                                                                                                    Sequence 7704, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRGANISM: Streptomyces avermitilis US-10-156-761-7704
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FURBENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1669
. LOCATION: (279)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1224
                                                                                                                                                                                                                                                                                                                                                                                                                      98 LY-IISSHLHFDHAGGNGAF---INT------PIIVQRAEYEA-AQHSEEYLKECIL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 PEDLLYIISSHLHFDHAGGNGAFI-----NTPIIVQRAEYEAAQHSEEYLKECILPNLNY 148
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                                                                                                                                                                                                                                                                                                                                                44 YLVGTGPRRILIDTGEP-----AIPE-----YISCLKOALTEFNTA 79
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                                                                                                                                                                                                                                                                           38 YLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDL
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                                                                                                                                Query Match
9.0%; Score 119; DB 9; Length 298;
Best Local Similarity 24.4%; Pred. No. 0.00096;
Matches 53; Conservative 31; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Score 109.5; DB 12; Length
21.8%; Pred. No. 0.0082;
Live 40; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 FENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGH 235
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----YMNSLKELLKIKADIIYPGH 209
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Sequence 9. Application US/10216163

Squence 10. US20030149239A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: ALIE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLC3
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT PHILKO DATE: 2002-08-09
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PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

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PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-31

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----NAETMLSSLDTV--LGLGDDTLLWPGHEYAEE 272
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; ORGANISM: Homo Sapien
US-10-216-163-8
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91 LFNGV----KVLPIPVLSDNYSYLIIDTQAQLAVAVDPSDPRAVQASIEKEGVTLVAILC 146 155 YEVVPGVQL--LHTPGHTPGHQSLLIETEK-----SGPVLLTIDASYTKENFENEVP 204 189 VVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPSCLFSGDLLFLSGCGRTFEG-----72; Length 361; Query Match
8.3%; Score 109; DB 12; Length 3
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 103 SHLHFDHAGGNGAFINTPIIVQRAEYEAAQHSEEYLKECI----205 FAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQF 240 63 LENGTFVEGQVLPKMTEEDRIVNIL-----KRVGYEPED PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-03-10
PRIOR PLING DATE: 1999-03-10
PRIOR PLING DATE: 1999-03-19
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PRIOR APPLICATION NUMBER: 60/14059
PRIOR PRILING DATE: 1999-06-27
PRIOR APPLICATION NUMBER: 60/14659
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PRIOR APPLICATION NUMBER: 60/14659
PRIOR PRILING DATE: 1999-06-37
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RIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-12-07
PRIOR PRILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR APPLICATION NUMBER: 60/169835 FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/119549
FILING DATE: 1999-02-10
APPLICATION NUMBER: 60/123618
FILING DATE: 1999-03-10 셤 ð g q ð

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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFRENCE: P3530PLC44
CURRENT APPLICATION NUMBER: US/10/219,063
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: (0/059113
PRIOR APPLICATION NUMBER: (0/059113
PRIOR APPLICATION NUMBER: (0/062287
PRIOR FILING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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33; Mismatches 62;
----NAETMLSSLDTV--LGLGDDTLLWPGHEYAEE 272
                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                                                     Sequence 8, Application US/10219063
Publication No. US20030187202A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 361
TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 49; Conserv
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US-10-219-063-8
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APPLICANT:
AUTILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1027
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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NUMBER OF SEQ ID NOS: 246
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----NAETMLSSLDTV--LGLGDDTLLWPGHEYAEE 272
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                                                                                                           Desnoyers, Luc
Gerritsen, Mary
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanbe, Colin L.
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US-10-219-067-8
; Sequence 8, Application US/10219067
Sequence 8, Application US/10219066 Publication No. US20030187203A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Conservative
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; ORGANISM: Homo Sapien
US-10-219-066-8
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Best Local Similarity
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RESULT 14
US-10-219-069-8
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APPLICANT:
APPLICANT:
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                                                                                                                                         APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE COLING
FILE REPERENCE: P3330PLC3.
CURRENT APPLICATION NUMBER: U0/119,480
PRIOR APPLICATION NUMBER: U0/06287
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063849
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1999-0-26
PRIOR FILING DATE: 1998-0-2-6
PRIOR APPLICATION NUMBER: 60/07924
PRIOR FILING DATE: 1998-0-2-6
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PRIOR APPLICATION NUMBER: 60/07924
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PRIOR APPLICATION NUMBER: 60/07924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Gaps
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; Sequence 8, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
Publication No. US20030187204A1
                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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Best Local Similarity
Matches 49; Conserv
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APPLICANT: STEPLAND. JOECOTIA L.
APPLICANT: STEPLAND. JOECOTIA L.
APPLICANT: STEPLAND. JOECOTIA L.
APPLICANT: WATANABE, COLIN L.
APPLICANT: WATANABE, COLIN L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/06213
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-26
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NUMBER OF SEQ ID NOS: 246
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                   Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030187206A1
GENERAL INFORMATION:
APPLICANT: Beancyers, Luc
APPLICANT: Deenoyers, Luc
APPLICANT: Gentiteen, Mary
APPLICANT: Geddard, Audrey
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-068-8
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                                                                        APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILER REPRESENCE: P3350P1640
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/06213
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-00-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030187207A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.7%;
Matches 49; Conservative 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapien
US-10-219-069-8
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 10530PLC52
CURRENT APPLICATION NUMBER: US/10/219,073
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/06213
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06913
PRIOR APPLICATION NUMBER: 60/06913
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07928
PRIOR PLING DATE: 1998-03-26
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TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 49; Conserv
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APPLICANT: Baker, Kevin P.
APPLICANT: Beanoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 20, 2004, 16:23:12; Search time 20 Seconds (without alignments) 1202.109 Million cell updates/sec

Title: Perfect score:

US-10-019-661-2 1315 1 MTVKKLYFVPAGRCMLDHSS.....VFFGHDIEQERGCKVFPEYI 250 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	crip	Zn-dependent hydro	conserved hypothet	hypothetical prote		Ω	Zn-dependent hydro	conserved hypothet			conserved hypothet	υ	` I		Н				ന	hypothetical prote			hypothetical prote	a	hypothetical prote	М			hypothetical prote	ρι
	DI	AG3176	G90312	G84288	D69438	D75552	AE3236	E82689	G75350	G89959	D69036	H70733	AH2652	E97434	D84057	A64337	T37060	F95386	AH0443	AF1276	AF1639	G69321	C83865	F72272	G71064	B75083	A84357	AG3085	B98201	F86942
	Length DB	1				271 2													275 2									Ŋ	35	51
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	Score	299	260	251	242.5	23	233.5	210	8	183.5	172.5	157	156.5	156.5	156	152	151	147	145.5	145.5	Н	43	143.5	143	143	141	141	141	141	139.5
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conserved hypothet	hypothetical prote	probable glyoxalas	conserved hypothet	hypothetical prote	conserved hypothet	conserved hypothet	conserved hypothet	conserved hypothet	metallo-beta-lacta	hypothetical prote	conserved hypothet	hypothetical prote		hypothetical prote	
E90315	E90473	F84719	A90269	D69811	G95282	C69468	G90423	G72321	AB3170	A75189	D75342	F71229	E83879	G69997	D84002
7	7	7	N	~	7	~	Ŋ	7	N	~	7	7	7	7	7
233	235	324	213	264	319	236	310	209	319	204	215	198	236	256	211
10.5	10.5	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.1	10.0	6.6	9.9	8.6	9.7
137.5	137.5	135.5	135	135	135	134.5	134.5	133.5	133.5	133	132	130.5	130.5	128.5	127
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Attestion: AG3176
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Query Match	atch	22.7%; Score 299; DB 2; Length 256;	
Matches	80	best botal Similarity 31.7%; Fred. NO. 1.48-17; Matches 80; Conservative 47; Mismatches 105; Indels 20; Gaps	8;
οχ	13	13 RCMLDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMP-ESAVNNEGLFNGTFVEG 71	7.1
QD	00		63
οy	72	72 QVLPKATEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTPIIVQRAEYEAA 131	131
Db	64	64 VYWPVIDKDGGCVDQIKALGFDPADVKYVVQSHLHIDHTGAIGRFPNATHIVQRSEYEYA 123	123
λŏ	132	132 QHSEEYLKECILPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIE 179	179
QQ	124		183
٥٨	180	180 TEKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFGHDI 237	237
Db	184	184 LPNSKPLLITIDAAYTLDHWE-EXALPGFLASTVDTVRSVQKLRTYAEKHDATVVTGHDP 242	242

à d RESULT 2 G90312 conserved hypothetical protein [imported] - Sulfolobus solfataricus

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hypotherical protein AF1509 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_charge 22-Oct-1999
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_charge 22-Oct-1999
C;Accession: D69438
R;Atenk, H.P.; Clayron, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson R;Atenk, H.P.; Clayron, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S Smith, H.O.; Woese, C.R.; Vener, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-262 «KLE»
A;Cross-references: GB:AE000998; GB:AE000782; NID:g2689321; PIDN:AAB89741.1; PID:g26490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Decology #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75552
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, F.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPEDLLYIISSHLHFDHAGGNGAFINTPIIVQRAEYEAA-----OHSEEYLKECILP--N 145
                                                                                        TPGHQSLLIETEK-SGPVLLIIDASYTKENFENEVPFA-GFDSELA--LSSIKRLKEVVM 225
                                                                                                                                                                                                 --EAAQHSEEYLKECILPNLNYKII----EGDYBVVPGVQLLHTPGH 169
  ---ADEHTLPAALADAGTAISDIDAVVASHLHLDHAGGLRHFAGTDTPIYVH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 PVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLP-KMTEEDRIVNILKRVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 PVYVWVIDGGDEKIVVDSGVEEA---KNGMFHG-----FPGKGGEKGLREAMEKVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ENEVPF--AGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQERGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 IQMTDTAGNTVEIPTSPLPFLPPGLHVDLSEWYESCFKALSVAKKANILPGHDPSLEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 INYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 29.5%; Pred. No. 7.8e-13;
Matches 72; Conservative 44; Mismatches 85
                                                                                                                                                                                                                                                                              226 KEKPIVFFGHD 236
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280 RTTADVFCGHD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262
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           111 FHHED---
                                                               125 RAEY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVFP
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84288
C;Accession: G84288
F;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc, Jung, K.H.; Alam, M.; Ferdias, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84288
A;Accession: G84288
A;Accession: Derliminary
                                                                                                M.J.; Chan-
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #sequence_revision 24-May-2001
C;Accession: G90312
R;She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90312
A;Accession: G90312
A;Molecule type: DNA
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A;Cross-references: GB:AE004437; NID:g10580853; PIDN:AAG19675.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1340C
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                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-269 <KUR>
A;Residues: GB:AE006641; NID:g13814770; FIDN:AAK41758.1; GSPDB:GN00155 C;Genetics: A;Gene: SS01537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 LHFDHAGGNGAFINT--PIIVQRAEYEAA-----QHSEEYLKEC--ILPNLNYKIIEGD 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 MIDHSSVNSTLIPG---ELLDLPVWCYLLETEEGPILVDTGMPESAVNNEG-----LFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 Y-EVVPGVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKE--NFENEVPFAGFDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.8%; Score 260; DB 2; Length 269; 29.4%; Pred. No. 2.8e-14; ive 49; Mismatches 98; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.4*
Matches 78; Conservative
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Matches 76; Conservative
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R.J.;

RI

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Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: 075350
R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation C; Genetics:
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                                                                      A,Cross-references: GB:AE001879; GB:AE000513; NID:g6457832; PIDN:AAF09759.1; PID:g645783
A,Experimental source: strain R1
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Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----WFSRTQTRLHYTEHDRLSRQMQRAGFDPAQVRVLLLTHLHIDHDRGMGDFPEAHLL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTPII 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 HTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENE----VPFAGFDSELALSSIKR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 VQRAE------YEAAQHSEFYLKECILPNLNYKIIEGDYEVVPGVQLL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE008690; PIDN:AAL46307.1; PID:g17744092; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 AGGNGAFINTPIIVQRAEYEAA-----QHSEEYLKECILPNL----NYKII---EGDY 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 VKSKFLRPEPQNLL--GSLRSFLDRQYSAPLPVWCWLIEHPSGLIVVDTGLTCTARSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Agrobacterium tumefaciens
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VKKLYFVPAGRCMLDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMPESAVNNEG
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                                                                                                                                                                                                                                                                                                    17.9%; Score 236; DB 2; Length 271; 27.0%; Pred. No. 2.9e-12; tive 50; Mismatches 100; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
A; Molecule type: DNA A; Residues: 1-271 < WHI>
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Best Local Similarity
Matches 76; Conserv
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A,Molecule type: DNA
A,Residues: 1-276 <KUR>
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A, Map position: 1
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A;Genome: plasmid
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                                                                                                                                                    C;Genetics:
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A'Experimental source: strain 9a5c
R'Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A. Briones, M.R.B.; Camargo, A.A.; Camargo, i.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Camargo, i.E.A.; Carraro, D.M.; Carrer, H. Submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre, Chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miraki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; Gellwick, C.F.M.; Miracca, E.C.; Miraki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; Balmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A.Huthors: as a Silva, A.C.R.; da Silva, A.C.; A. Silva Jr., Wa.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.R.Eference number: AS9328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein XF1361 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Saces:18-4049-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82689
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 406, 151-157, 2000
A;Fitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MulD:2036517; PMLD:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-279 <SIM>
A,Residues: 1-279 <SIM>
A,Cross-references: GB:AE003968; GB:AE003849; NID:g9106363; PIDN:AAF84170.1; GSPDB:GN001:
207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 IGPQLLAKNIDPSRDVEAVILTHMHDHAGGLDHFPHTRIIVTKENYDASRGFFGRVAGC 154
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                                                                                                                                                                                                                            208 FDSELALSSIKRLKEVVMKEKPIVFFGHDIEQ
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R.J.; F C.; Ma}

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Appothetical protein Rv2300c - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Bate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C,Accession: H70733
R,Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S, Connor, R.; Davies, R.; Parkhill, T.; Geneles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A,Authoris: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500; MUID:98295987; PMID:9634230
A,Accession: H70733
A,Accession: H70733
A,Residues: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-2100 CCCL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 11.9%; Score 157; DB 2;
1. Similarity 25.7%; Pred. No. 1.4e-05;
62; Conservative 34; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 62; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: MTH1267
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S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Acference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75350
A;Accession: G75350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <HHF>
A;Coss.references: GB:AE002022; GB:AE000513; NID:g6459590; PIDN:AAF11372.1; PID:g645959
A;Experimental source: strain R1
A;Gene: DR1823
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein SA1568 [imported] - Staphylococcus aureus (strain N315) C; Species: Staphylococcus aureus C; Species: Staphylococcus aureus C; Species: 10-May-2001 #text_change 22-Oct-2001 C; Date: 10-May-2001 #text_change 22-Oct-2001 R; Microda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Application of A; Active: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 HIHFDHAG-----GNGAFINTPIIVQRAEYEAAQHSEE-----YLKECILPNIN---YK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 LVDGETELLPGLSVLPLPGHNLGQQGVVL---RSGGQTLVYVADLVPTTAHAPYEYVMGY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 ILVDIGMPESAVNNEGLFNGTFVEGQVLPKM---TEEDRIVNILKRVGYEPBDLLYIISS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 IIEGDYEVVPGVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENEVPFA-GF 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 LDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYEPEDLLY11SSHLHFDHA-----GGNGAFINTPIIVQRAEYEAAQHSEEYLKECILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 TIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.0%; Score 183.5; DB 2; Length 280; Best Local Similarity 23.7%; Pred. No. 7.5e-08; Matches 55; Conservative 48; Mismatches 76; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                            Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                          14.1%; Score 186; DB 2; 27.1%; Pred. No. 4e-08;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.1%; Pred. No. 4e-08
Matches 49; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 VLVETGMWDRG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-280 <KUR>
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11;

Gaps

58;

87; Indels

Length 310;

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(strain De
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A,Reference number: A69000; MUID:98037514; PMID:9371463
A,Accession: D69036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000893; GB:AE000666; NID:g2622375; PIDN:AAB85756.1; PID:g26223E
A;Experimental source: strain Delta H
                                                                                                                                                                             conserved hypothetical protein MTH1267 - Methanobacterium thermoautotrophicum (strain longeries: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: D69036
R;Smith, D.R; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Iki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 KRVGYEPEDLLYIISSHIHFDHAGGNGAFINTPIIVQRAEYEAAQHSEE----YLKECI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-205 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 GELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNIL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 LPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENE
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--KERMIPYF---1000 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cch 13.1%; Score 172.5; DB 2; Length 2
al Similarity 26.3%; Pred. No. 4e-07;
56; Conservative 39; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 VPFAGFDSELALSSIKRLKEVVMKEKPIVFFGH 235
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: : : | : : | |: 203 HMGDIFPTTAHKNPLWVTAYD-DYPMQSIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: glyoxalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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12;

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Pypothetical protein BH3260 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Dace-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D84057
R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A;Reference number: A83650; MUID:20512582; PMID:11058132
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Acces 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumm A;Reference number: A97359; MUID:21608551; PMID:11743194
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A;Nolecule type: DDA
A;Residues: 1-284 <STO>
A;Residues: 1-284 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06979.1; GSPDB:GN001
A;Experimental source: strain C-125
A;Genetics:
A;Gene: BH3260
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE007869; PIDN: AAK86430.1; PID: g15155568; GSPDB: GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 RAEYE-----AAQHSEEYLKECILPNLNYKIIEGD-YEVVPGVQLLHTPGHTPGH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 QSLLIETEKSGPVLLTIDASYTKENF-----ENEVPFAGFDSELALSSIKRLKEVVMK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 EGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAG-----GNGAFINTPIIVQ 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 STLTPGELLD------LPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 LLYIISSHLHFDHAGG-----NGAFINTPIIVQRAEYEAAQHSEEYLKECILPNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%; Score 156.5; DB 2; 24.9%; Pred. No. 2e-05; iive 39; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 156; DB 2; 25.9%; Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: AGR C 1105
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: : | |:
DR-LPFLGY 342
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Best Local Similarity
Matches 43; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <KUR>
                                                                                                                                                                                                                                                                                            A; Accession: E97434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D84057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2322, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metallo-beta-lactamase superfamily protein [imported] - Agrobacterium tumefaciens (strai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AGR_C_1105 [imported] - Agrobacterium tumefaciens (strain C58, Cere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                             180 QWAHGPKLVEHGPDGEPWRGFASAKPLDSIGTGVVLVPMPGHTRGHAAVAVDAGHRW-VL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                        92 YEPEDLLYIISSHLHFDHAGGNGAFINTPIIVQRAEYEAAQHSEEYLKECILPNLNY--- 148
                                                                                                                                                                                                                                                                                 ------GVQLLHTPGHTPGHQSLLIETEKSGPVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-333 «KUR»
A;Cross-references: GB:AE008688; PIDN:AAL41638.1; PID:g17738978; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                        125 RAEYE-----AAQHSEEYLKECILPNINYKIIEGD-YEVVPGVOLLHTPGHTPGH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 OSLLIETEKSGPVLLTIDASYTKENF------ENEVPFAGFDSELALSSIKRLKEVVMK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAG-----GNGAFINTPIIVQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 SAETVGKLLEDNFLPKDQFVNSFSPV---LINTGSDLVLFDTGFGEA---GRGAGNGRLT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLTPGELLD------LPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Agrobacterium tumefaciens
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
LLETEEGPILVDTGM-----PESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVG
                                                                                                                                                                                                                                                                                                                                                                                                                          188 LTIDASYTKENFEN--EVPFAGFDSELALS-----SIKRLKEVVMKEKP--IVFFGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.9%; Pred. No. 1.8e-05;
Matches 62; Conservative 39; Mismatches 85; Indels 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A,Gene: Atu0622
A,Map position: circular chromosome
                                                                                                                                                                                                                                                                                 ----KIIEGDYEVVP--
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DR-LPFLGY 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: AH2652
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                 149
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38;

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hypothetical protein MJ0296 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Datcession: A64337
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; White, D.S.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G.A;Tilte: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64307
A;Accession: A64337
A;Accession: A64337
A;Accession: A64304
A;Residues: 1-203 <BUL>
A;Residues: 1-203 <BUL>
A;Residues: 1-203 <BUL>
A;Cross-references: GB:U67484; GB:L77117; NID:g1591009; PIDN:AAB98284.1; PID:g1591018; T
C;Genetics:
A;Map position: FORZ79752-280363
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 PGVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENEV-PFAGFDSELALSSI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 --IEIIETPGHTYGSISVIXK-----DYVVVGDASPLKNNILKMIPPKLNVDEKLALESL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 YIISSHIHFDHAGGNGAFINTPIIVQRAEYEAAQHSEEYLKECILPNINYKIIEGDYEVV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 LLETEEGPILVDIGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.6%; Score 152; DB 2; Length 203; Best Local Similarity 24.3%; Pred. No. 2.1e-05; Matches 49; Conservative 34; Mismatches 63; Indels
                            147 ----NYKII-----EGDYEVVPGVQLLHTPGHTPGHQSLLIETE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 KRLKE-----VVMKEK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 KKIRKLRKNVITGHEGIVYKEK 201
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Search completed: February 20, 2004, 16:26:33 Job time : 21 secs

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using sw model protein search, OM protein

February 20, 2004, 16:24:07; Search time 21 Seconds Run on:

(without alignments) 503.701 Million cell updates/sec

US-10-019-661-2 1315 1 MTVKKLYFVPAGRCMLDHSS.....VFFGHDIBQERGCKVFPEYI 250 Title: Perfect score:

Sequence:

BLOSUM62 Scoring table:

328717 seqs, 42310858 residues Gapop 10.0 , Gapext 0.5 Searched:

328717 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PacKfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			24102, A		174, AD	537, AD	3490, A	62, Appl	2, Appl	S. Appl	62, Appl	2, Appl	2, Appl	Appl	Appl	9680. A	945, App	541, Ap	749, Ap	8, Appli	Appli	144, Ap	28, Appl	Appli	27. App	4, Appl	
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Description	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
ID	US-09-328-352-5381	-352-5	US-09-252-991A-24102	991A-2057	US-09-107-532A-5174	-001C-	US-09-252-991A-18490	-713D-	US-08-835-268-62	US-09-060-692-62	US-08-833-391-62	US-09-060-610-62	PCT-US94-10151A-62	US-08-738-944-50	US-09-263-352-40	US-09-252-991A-29680	US-09-198-452A-945	134-001C-564	US-09-107-532A-6749	8	US-09-612-473-8	US-09-328-352-5144	US-08-506-296B-28	US-08-471-119A-2	US-09-564-805-227	US-08-231-193A-54	US-08-486-273A-54
DB	4	4	4	4	4	4	4	Н	Н	7	m	4	Ŋ	Н	ო	4	4	4	4	'n	4	4	4	7	4	7	7
% Query Match Length	311	326	722	295	239	209	290	724	724	724	724	724	724	262	262	217	265	440	515	254	254	704	1268	15281	4	1214	1214
% Query Match	13.7	10.1	7.6	8.9	8.7	8.1	7.7	6.9	6.9	6.9	6.9	6.9	6.9	6.8	6.8		9.9	6.5		6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3
Score	180	132.5	128	117.5	114.5	106	101	90.5	90.5	90.5	90.5	90.5	90.5	89	88	88.5	86.5	85.5		84		84		84	ъ.	83.5	œ.
Result No.	П	7	е	4	τŪ	9	7	80	σ	10	11	12	13	14	15	16	17		19		21	22	23		25	26	27

Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	App1	App1	Appl	Appl	Appl	Appl	Appl
Sequence 54,	Sequence 54,	Sequence 54,	Sequence 54,		Sequence 54,		Sequence 50,	Sequence 50,					Sequence 50,	Sequence 48,	Sequence 48,		
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US-08-480-474-54	US-08-940-086A-54	US-08-940-035A-54	US-08-935-105A-54	US-09-648-797-54	US-09-386-123-54	US-08-231-193A-50	US-08-486-273A-50	US-08-480-474-50	US-08-940-086A-50	US-08-940-035A-50	US-08-935-105A-50	US-09-648-797-50	US-09-386-123-50	US-08-231-193A-48	US-08-486-273A-48	US-08-480-474-48	US-08-940-086A-48
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6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3
83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 5381, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE GTC99-0394
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
NUMBER OF SEQ ID NOS: 8252
LENGTH: 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 IETEKSGPVLLIIDASYT--KENFEN------EVPPAGFDSELALSSIKRLKEVVMKE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 CYLLETEEGPILVDTGMPESAVNNEGLFN-----GTFVE--GQVLPKMTEEDRIVNI
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            13.7%; Score 180; DB 4; Length 311; 27.1%; Pred. No. 6.5e-11; Live 42; Mismatches 72; Indels 7
                                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii
US-09-328-352-5381
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Best Local Similarity
Matches 69; Conserv
RESULT 1
US-09-328-352-5381
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228 KPI-VFFGHDIEQER 241

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Sequence 5506, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERGGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20572
LENGTH: 295
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Sequence 5174, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLLTIDASYTKENFENEVPFA-----GFD--SELALSSIKRLKEVVMKEKPIVFFG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 RDRASFVPELLDILQASGRLELLDDGERSAHLGEGWRFHFSEGHTPG-QMLPEIAMPDGP
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                              -LTIDASYTKENFEN--
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                                                                                                                                                          ----FAGFDSELALSSIKRLKEVVMKEKPIVFFGHD 236
                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
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                           163 LLHTPGHTPGHQSL---LIETEKSGPVL-
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 20572, Application US/09252991A; Patent No. 6551795
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STATE: Massachusetts
COUNTRY: USA
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US-09-107-532A-5174
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Best Local &
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Sequence 24102, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRICR PAPPLICATION NUMBER: US 60/074,788
PRICR FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 PIIVQRAEYE------AAQHSEEYL-----KECILPNLNYKIIE--GDYEVVPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFENEVPFAGFD----SELALSS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : | | : | | : | 105TIYLDPKLFKALSPAEKTKILT----KYAAVNEKGIQTSVNAFLVDDGKSLTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 VDSGAASCFGPQL---GSİAKNLELAĞYQLANVKTVLLTHLHPDHVCGIAQNGKAVFPNA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 TIYAHERBADYWLNPANEKTVPADKKENYLGTVKNVKAALAPYQAKKAFKTFKDGDVIOG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 FEVINTQGHTPGHHSFRLKSK--GQQIVFVGDIVHSHSLQFDAPKTGVDFDVNSEQAINT 277
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                                                                                                                                                                                                                                                                                                                                                                      10.1%; Score 132.5; DB 4; Length 326; 23.2%; Pred. No. 8.1e-06;
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5506
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9.7%; Score 128; DB 4; Length 722;
Best Local Similarity 24.1%; Pred. No. 8.2e-05;
Matches 67; Conservative 29; Mismatches 72; Indels 1
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-----VQGRERDVLVDSG
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                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 23.2%
Matches 62; Conservative
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US-09-252-991A-24102
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARENGINCAR FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 IVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFI---NTPIIVQRAEYE-----AA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 --TFVEGOVLPROMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTPIIVQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 RAEYEAAQHSEEYLKECILPN-----LNYKI-------IEGDYEVVPGVQL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 WAPYEEIAFSRIATPPAAFPSQFRHGVRWRPYSFDPRPFMGFDESLDLFGDGRLV---L 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFE--NEVPFAG-----FDSELALSS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 VPLPGHTPGSVGLFVTLDSGRRLFFSGDTSWRLEGVEGPROKFFAGRALVDRDPARTLAQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 STLTPGELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDR 82
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    8.1%; Score 106; DB 4; Length 209;
l Similarity 25.0%; Pred. No. 0.0028;
42; Conservative 26; Mismatches 56; Indels
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7.7%; Score 101; DB 4; Length 290;
Best Local Similarity 20.7%; Pred. No. 0.016;
Matches 57; Conservative 37; Mismatches 106; Indels
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           PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3637
LENGTH: 209
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                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3637
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Best Local 9
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ORGANISM:
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Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REPERRNCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KKLYFVPAGRC--MLDHSSVN-----STLTPGELLDLPVWCYLLETEEGPILVDTG 52
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8.7%; Score 114.5; DB 4; Length 239;
Best Local Similarity 21.4%; Pred. No. 0.00042;
Matches 62; Conservative 43; Mismatches 80; Indels 105
COMPUTER NELLEL
MEDITUM TYPE: CD/RUM 1555.
COMBUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PSCII
CURRENT APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/08151
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: 011y 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPAN: (781)893-8077
TELEPAN: (781)893-8277
INFORMATION FOR SEQ ID NO: 5174:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...239;
SEQUENCE DESCRIPTION: SEQ ID NO: 5174:
US-09-107-532A-5174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ---NGAFINTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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US-09-134-001C-3637
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GENERAL INFORMATION:
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484 KLLDIFEVAPNEALQVWEI---SQTRKSLYIGTDHR---IKQIDLAMCNRRYDNCFRCVR 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VMKEKPIVFFGHDIEQERGCKV-FP 247
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MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: TEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-193
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 94-002-1
REFERENCE/DOCKET NUMBER: 94-002-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                        Sequence 6.2, Application US/08121713D
Sequence 6.2, Application US/08121713D
Patent No. 5639866
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Matthes, David
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APPLICANT: Matthes, David
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APPLICANT: APPLICANT: Timothy
CORRESPONDENCE ADDRESS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 22.2%
Watches 54; Conservative
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ZIP: 94104
                    RESULT 8
US-08-121-713D-62
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Sequence 62, Application US/08835268 Patent No. 5807826

RESULT 9 US-08-835-268-62

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61 EGLFWGTFVEGQ-----VLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFD---- 108
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484 KLLDIFEVAPNEALQVMEI---SQTRKSLXIGTDHR---IKQIDLAMCNRRYDNCFRCVR 537
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                                                                                                                                                                                                                                                                                                      ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex I.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              E: SCIENCE & TECHNOLOGY LAW GROUP
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENI INFORMATION:
NAME: OSMAIL, RICHARDA A.
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-060-692-62; Sequence 62, Application US/09060692; Patent No. 5935865; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 343-4342
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                                                                                                                                                                                                                                             CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 54; Conserva
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                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                        STATE:
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Kolodkin, Alex L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 HEHNNPVYYKRDLVFTKLVVDKIRIDIL--NQEYIVYYGTNLGRIYKIVQYYRNGESLS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 VPFAGFDSELALS---SIKRLKEV------VMKEKPIVFFGHDIEQERGCKV-FP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EGLFNGTFVEGQ------VLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFD----
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                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
                                                 APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200 CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-5EP-1993
ATTORNEY AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTATION NUMBER: 36.627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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%Sequence 62, Application US/08833391

%Patent No. 6013781

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.
Goodman, Corey S.
Kolodkin, Alex L.
Matthes, David
Bentley, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 62:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.2'
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                        COUNTRY:
                   APPLICANT:
APPLICANT:
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61 EGLFNGTFVEGQ-----VLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFD---- 108
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                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
6.9%; Score 90.5; DB 3;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87;
APPLICANT: Matthes, David
APPLICANT: Matthes, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'CONDOY, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SEP-193
ATTORNEY/AGENI INFORMATION:
NAME: OSMAIN, Richard A.
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/09060610; Patent No. 634454
GENERAL INFORMATION: APPLICANT: ROLOGENIA, Alex L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 724 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
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87; Indels
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Patent No. 5783431
GENERAL INFORMATION:
APPLICANT: Peterson, et al.
TITLE OF INVENTION: BCREENING NOVEL METABOLIC PATHWAYS
NUMBER OF SEQUENCES: 51
COMMERSPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                     CORPLOYER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10151A
FILING DATE: 13-SEP-1994
CLASSIFICATION NUMBER: PCT/US94/10151A
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REFSERNCE/DOCKET NUMBER: 36,627
REFSERNCE/DOCKET NUMBER: PF-58750-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELERA: 910 277299 FHT UR
INFORMATION FOR SEQ ID DO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TTYPE: amino acid
TTYPE: amino acid
    FLEHR HOHBACH TEST ALBRITTON & HERBERT Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%; Score 90.5; DB 5;
22.2%; Pred. No. 0.83;
live 39; Mismatches 87;
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1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.2*
Matches 54; Conservative
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COMPUTER READABLE FORM:
                     STREET: 4 billour
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                                                                                             RY: USA
94111-4187
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US-08-738-944-50
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                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | : | : | : | 426 HEHNNPVYYKRDLVFTKLVVDKIRIDIL--NQEYIVYYGTNLGRIYKIVQYYRNGESIS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 QAAFNGKFKEQSSSNSAWLPVLNSRVPEPRPGTCVNDTSNLPDTVLNFIRSHPLMDKAVN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 HAGGNGAF----INTPIIVQRAEYEAAQHSEEYLKECILPNLN--YKIIE----GD--- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 ----YEVVP--GVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFEN----E 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 KLLDIFEVAPNEAIOVMEI---SOTRKSLYIGTDHR---IKOIDLAMCNRRYDNCFRCVR 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 VPFAGFDSELALS---SIKRLKEV------VMKEKPIVFFGHDIEQERGCKV-FP 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Indels 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.9%; Score 90.5; DB 4; Length 724; Best Local Similarity 22.2%; Pred. No. 0.83; Matches 54; Conservative 39; Mismatches 87; Indels 63
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GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSE:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPRAX: (415) 343-4342
                                                                                                                                                                                                                                                          ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,268
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-060-610-62
                                                                                                                                                                      STREET: 268 Bush Sti
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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61 EGLENGTFVEGQ-----VLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFD---- 108
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                                                                                                                                                                                                                                                                                                                               426 HEHNNPVYYKRDLVFTKLVVDKIRIDIL--NQEYIVYVGTNLGRIYKIVQYYRNGESLS 483
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484 KLLDIFEVAPNEAIQVMEI---SQTRKSLYIGTDHR---IKQIDLAMCNRRYDNCFRCVR 537
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                                                                                                                                                                                                                                                                                                                                                                                                                            -----YEVVP--GVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYTKENFEN----E 202
                                                                      Gaps
                                                                  63;
Length 724;
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US-09-263-352-40
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Patent No. 624211

GENERAL INFORMATION:

APPLICANT: Peterson, T.

APPLICANT: Peterson, T.

APPLICANT: Peterson, T.

TITLE OF INVENTION: METHODS FOR GENERATING AND SCREENING NOVEL METABOLIC

TITLE OF INVENTION: METHODS FOR GENERATING AND SCREENING NOVEL METABOLIC

TITLE OF INVENTION: PHHMAYS

FILE REFERENCE: 8757-010

CURRENT APPLICATION NUMBER: US/09/263,352

CURRENT FILING DATE: 1999-03-05

EARLIER PILING DATE: 1997-12-05

MUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 40

LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 LYIISSHLHFDHAGGNGA-----FINTPIIVQRAEYEAAQHSEEYLKECILPNLNYKI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 TGESTLVIPTSIILHQQTRTFGDTEVEFVFANDGHSPGDVMALPKQR-----ILIGGDV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TPGHTPGHQSLLIETEKSGPVLLTIDASY 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 YLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 RWVVNSHSHADHWLGNAALAKLGAELISTSLSAETMKSDGPVDVKAFF-----NMTKGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.8%; Score 89; DB 1; Length 262; Best Local Similarity 19.9%; Pred. No. 0.25; Matches 44; Conservative 33; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 TKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGH 235
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 IEGDYEVVPGVQLLH-----
                                                                                                                                                                                                                                                                                                                                                                             262 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CXC-AMN20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1...262;
COTHER INFORMATION:
US-08-738-944-50
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US-09-263-352-40
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                                                                                          38 YLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDL 97
                                                                                                                              39 RWVVNSHSHADHWLGNAALAKLGAELISTSLSABTMKSDGPVDVKAFF-----NMTKGA 92
                                                  62; Gaps
6.8%; Score 89; DB 3; Length 262; 19.9%; Pred. No. 0.25;
                                               82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     | : | : | : | 148 VNSNFMPIMTPRGNITQL----ISVLKEVEQLSPLIVLTGH 184
                                                                                                                                                                                                                                                                                                                                                                                          195 TKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGH 235
                                               33; Mismatches
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Job time: 22 secs
                                                                                                                                                                                                                                                                                          151 IEGDYEVVPGVQLLH----
                                               44; Conservative
  Query Match
Best Local Similarity
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February 20, 2004, 16:18:56; Search time 41 Seconds (without alignments) 967.845 Million cell updates/sec
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1315
1 MTVKKLYFVPAGRCMLDHSS.....VFFGHDIEQERGCKVFPEYI 250
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2: /SIDSI/gcgdata/geneseqp-embl/AA1981.DAT:*
2: /SIDSI/gcgdata/geneseqg-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1982.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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    protein search,

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Perfect score:
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                                                                                                         OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*/SIDS1/gcgdata/geneseqy/geneseqp-embl/AA2003.DAT:* 99... 111... 112... 114

SUMMARIES

| SIDS1/gegdata/geneseq/geneseqp-embl/AA1990.DAT:
| SIDS1/gegdata/geneseq/geneseqp-embl/AA1990.DAT:
| SIDS1/gegdata/geneseqg-embl/AA1991.DAT:
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| SIDS1/gegdata/geneseqg-geneseqp-embl/AA1993.DAT:
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| SIDS1/gegdata/geneseqg-geneseqp-embl/AA1990.DAT:
| SIDS1/gegdata/geneseqg-geneseqp-embl/AA1990.DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

Description	Listeria sp. str	Bacillus sp. Au	Autoinducer inacti	Autoinducer ina	Autoinducer ina	Autoinducer inac	Autoinducer inac	Autoinducer inac	100000000000000000000000000000000000000
ΙD	1	AAU78814	AAU78808	AAU78807	AAU78804	AAU78806	AAU78809	AAU78811	
DB	22	23	23	23	23	23	23	23	
f Query Match Length DB	250	248	250	250	250	250	250	250	
Query Match	100.0	99.2	94.6	93.4	92.7	92.2	92.2	92.2	
Score	1315	1304	1244	1228	1219	1213	1212	1212	0000
Result No.	1	71	м	4	Ŋ	9	7	80	•

New bacterial autoinducer inactivation proteins and nucleic acids encoding the protein, for increasing disease resistance, preventing or

N-PSDB; AAF29642

Autoinducer inacti		Autoinducer inacti	Listeria monocytod	Putative P. abyssi	Burkholderia cépac	Arabidopsis thalia	Arabidopsis thalia	Putative P. abyssi	Human polypeptide	Listeria monocytog	Amino acid sequenc	Human prostate tum	Human cancer assoc	Novel human enzyme	Human protein sequ	Human MDDT SEQ ID	Arabidopsis thalia		Arabidopsis thalia	ß		w	Arabidopsis thalia	Lactococcus lactis	Human Hydrolase pr	Human PRO protein,	Human protein SEQ	Drosophila melanog	Staphylococcus epi	Drosophila melanog	Drosophila melanog	Human NOV17d prote	Arabidopsis thalia	Arabidopsis thalia	Human NOV17b prote
AAU78805	AAU78812	AAU78815	ABB48771	AAB96283	AAB73541	AAG30597	AAG30596	AAB96055	ABB90340	ABB49158	AAB67569	AAY73880	AAB43779	AAU23487	AAM25792	ABP51438	AAG10298	AAG10299	AAG10300	AAG41447	AAG41446	AAG41445	AAG31661	ABB53851	AAY71110	AAU83595	AAM78721	ABB64252	ABP38792	ABB67381	ABB71300	ABU65074	AAG10987	AAG10986	ABU65072
23	23	23	23	22	22	21	21	22	23	23	22	20	21	22	22	23	21	21	21	21	21	21	21	23	21	23	22	22	23	22	22	23	21	21	23
250	250	263	283	222	281	285	324	204	285	238	288	298	298	298	298	323	331	288	220	281	286	331	252	210	361	361	385	228	209	271	305	282	258	268	282
91.4	91.3	23.7	11.1	10.7	10.3	10.3	10.3	10.1	9.4	9.1	0.6	0.6	0.6	9.0	0.6	9.0	8.9	8.9	8.7	8.7	8.7	8.7	9.8	8.5	8.3	8.3	8.3	8.2	8.1	8.0	8.0	7.8	7.7	7.7	7.7
1202	1200	311	145.5	141	135.5	135.5	135.5	133	123.5	119.5	119	119	119	119	119	118.5	117.5	117	115	114.5	114.5	114.5	113.5	112	109	109	109	108	106	105	105	102.5	101.5	101.5	101.5
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Listeria; AilA; autoinducer inactivation protein A; antibacterial; disease resistance; soft rot disease resistance; bacterial infection. (MOLE-) INST MOLECULAR AGROBIOLOGY 1 RES LINK. AAB50476 standard; Protein; 250 AA Listeria sp. strain 240Bl AiiA. Jinling 99WO-SG00128. 99SG-0003146. (first entry) Lian-Hui Z, Yihu D, WPI; 2001-138146/14. WO200102578-A1. 17-NOV-1999; 02-JUL-1999; 10-APR-2001 Listeria sp. 11-JAN-2001. AAB50476; AAB50476 THE STATE OF THE S

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The present sequence is a bacterial autoinducer inactivation protein (AilA). It is useful for increasing disease resistance as well as preventing or reducing bacterial damage to a plant or animal. The nucleic acid encoding the AilA protein may be used to confer resistance to diseases where expression of pathogenic genes are regulated by autoinducers, such as diseases caused by pseudomonas aeruginosa, Erwinia stewatii, Xenorhabdus nematophilus, Erwinia chrystauthemi, Pseudomonas solanacearum and Xanthomonas campestris. It may also be used to confer soft rot disease resistance in susceptible plants such as potato, eggplant, Chinese cabbage, carrot and celery. The bacterial autoinducer infections in animals including humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IIVQRAEYEAAQHSEEYLKECILPNINYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
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reducing bacterial damage to a plant or animal, or treating bacterial
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                            DB 22; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autoinducer inactivation; AilA; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                              100.0%; Score 1315; DB 22; 100.0%; Pred. No. 1.6e-134;
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                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                   Claim 6; Fig 4B; 49pp; English.
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                    infections in animals
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                                                                                                                                                                                                                                                                                                 Sequence
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Best Local
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Gaps

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autoinducer (N -ageline autoine) inactivation protein. The autoinducer (N -agyl-homoserine latcine) inactivation protein. The complaints of autoinducer is useful for increasing disease resistance in a plant or animal by introducing a polymuclectide into a cell of such a plant or animal by introducing a polymuclectide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein of suseful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial bicilins, by exposing consistent of the autoinducer inactivation protein. A characterial cell transformed with the polymuclectide, especially a plant or animal bacterium preferably Bacillus thuringiansis which is from Bl. B2, conting a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This is the amino acid sequence of the Bacillus sp. 240Bl autoinducer inactivation protein. Aim, a putative metallohydrolase and autoinducer inactivation protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                          Polymucleotide encoding autoinducer inactivation protein, bacterium having polymucleotide, and protein useful for increasing resistance a disease in sustainable plant or animal and for reducing bacterial
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.2%; Score 1304; DB 23; Length 248; 100.0%; Pred. No. 2.5e-133; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autoinducer inactivation; Alig; N-acyl-homoserine lactone; disease resistance; Dacterial damage reduction; biofilm; potato soft rot disease; Erwinia carotovora.
                                                                                                                                                   The invention describes an isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Autoinducer inactivation protein AiiG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78808 standard; Protein; 250 AA
                                                                                                                 Example 2; Fig 6; 82pp; English
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Best Local Similarity 100.0
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WPI; 2002-304123/34.
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240

240

180

23-AUG-2000; 2000WO-SG00123

resistance; bacterial damage reduction; biofilm;

potato soft rot disease; Erwinia carotovora

disease

Bacillus thuringiensis B17

WO200216623-A1 28-FEB-2002 (MOLE-) INST MOLECULAR AGROBIOLOGY

t Q

WPI; 2002-304123/34.

N-PSDB; ABK47471

encoding

Zhang L, Dong Y,

23-AUG-2000; 2000WO-SG00123 23-AUG-2000; 2000WO-SG00123

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autoinducer (N-acyl-homoserine lactone) inactivation protein. The autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably comman; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A capacterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, animal bacterium preferably Bacillus thuringiensis which is from B1, B2, disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This is the amino acid sequence the autoinducer inactivation protein converse.
                                                                                                                                                                                     Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance a disease in sustainable plant or animal and for reducing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Autoinducer inactivation; AiiF; N-acyl-homoserine lactone;
                                                                                                                                                                                                                                                                                                         The invention describes an isolated polynucleotide
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                                23-AUG-2000; 2000WO-SG00123
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les 232; Conservative
                                                                                                      Dong Y, Xu J;
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                                                                                                      Zhang L,
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                                                                             EGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTP
                                                            1 MIVKKLYFVPAGRCMLDHSSVNSTLIPGELLDLPVWCYLLETEEGPILVDTGMPESAVNN
                                                                                                                                                                                                          EKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQE
                                                                                                                                                                                                                                                                 0; Gaps
94.6%; Score 1244; DB 23; Length 250; 92.8%; Pred. No. 8.7e-127; Live 13; Mismatches 5; Indels 0
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RESULT 5 AAU78804

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The invention describes an isolated polymucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The autoinducer (N-acyl-homoserine lactone) inactivation protein. The polymucleotide is useful for increasing disease resistance in a plant or animal by introducing a polymucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A caries animal bacterium preferably Bacillus thuringiensis which is from B1, B2, B1, B1, B2, B2, B2, B2, B2, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.

This is the amino acid sequence of the autoinducer inactivation protein activity of which is studied in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Fig 9; 82pp; English
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les 232; Conser
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The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A bacterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B2 and B25, is useful for increasing resistance to disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. poctato soft rot disease caused by Brwinia carotovora. This is the amino acid sequence of the autoinducer inactivation protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance a disease in sustainable plant or animal and for reducing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.7%; Score 1219; DB 23; Length 250; 91.2%; Pred. No. 4.6e-124;
                                                                                                                               Autoinducer inactivation, AifC; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                  potato soft rot disease; Erwinia carotovora.
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                                                                                                 Autoinducer inactivation protein AilC
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standard; Protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Fig 8; 82pp; English.
                                                                                                                                                                                                                                                                                                    23-AUG-2000; 2000WO-SG00123.
                                                                                                                                                                                                    Bacillus thuringiensis Cotl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK47468
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The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The autoinducer (N-acyl-homoserine lactone) inactivation protein. The call autoinducer is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein canneal, in a manner that allows the cell to express the gene. The protein burnal, in a manner that allows the cell to express the gene. The protein contains and for reducing bacterial damage to a plant or animal pacterial cell transformed with the polynucleotide, especially a plant or bacterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, animal bacterium preferably Bacillus thuringiensis which is from B1, B2, disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.

This is the amino acid sequence of the autoinducer inactivation protein contains the amino acid sequence of the autoinducer inactivation protein activity of which is studied in the
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181 EKSGVVLLTIDASYTKENFEDEVPFAGFDPELALSSIKRLKEVVMKEKPLVFFGHDIEQE 240
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                                                                                                                                                                                                                                                                                                                             Autoinducer inactivation, AiiE; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm;
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                                                                                                                                                                                                                                                                                                                                                                     potato soft rot disease; Erwinia carotovora.
                                                                                                                                                                                                                                                                                               Autoinducer inactivation protein AilE.
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                                                                                                                                                                               AAU78806 standard; Protein; 250 AA.
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                                               241 RGCKVFPEYI 250
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N-PSDB; ABK47470.
                                                                                 241 KGCKVFPEYI
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92.2%; Sco 90.8%; Pre tive 13;

Best_Local Similarity 90.8 Matches 227; Conservative

Query Match

Length 250;

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EGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTP

EKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQE

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EKSGPVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQE
                                                                                          IIVQRAEYEAAQHSEEYLKECILPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET
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KSCRVFPEYI 250
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N-PSDB; ABK47473.
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The invention describes an isolated polynuclectide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynuclectide is useful for increasing disease remistance in a plant or animal by introducing a polynuclectide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A bacterial cell transformed with the polynuclectide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, animal
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                                                                                                                                        Autoinducer inactivation, AilJ; N-acyl-homoserine lactone; disease resistance; bacterial damage reduction; biofilm;
                                                                                                                                                                                 potato soft rot disease; Erwinia carotovora.
                                                                                                        Autoinducer inactivation protein AiiJ
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AAU78811 standard; Protein; 250 AA.
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                                                                                                                                                                                                                   Bacillus thuringiensis B22.
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang L, Dong Y, Xu J;
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N-PSDB; ABK47475.
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                                                                       18-JUN-2002
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Claim 17; Fig 9; 82pp; English.

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B17, B18, B20, B21, B22 and B25, is useful for increasing recommended by disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This is the amino acid sequence of the autoinducer inactivation protein AilJ, the autoinducer inactivation activity of which is studied in the
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                                                                                                                        Query Match 92.2%; Score 1212; DB 23; Best Local Similarity 90.8%; Pred. No. 2.7e-123; Matches 227; Conservative 13; Mismatches 10;
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KGCRVFPEYI 250
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N-PSDB; ABK47474.
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                                                                                                  250 AA;
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(N-acyl-homoserine lactone) inactivation protein. The
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                                                                                                                                                 91.9%; Score 1209; DB 23; 90.8%; Pred. No. 5.7e-123; iive 12; Mismatches 11;
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Best Local Similarity 90.8
Matches 227; Conservative
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N-PSDB; ABK47469.
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KGCRVFPEYI
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                                                                                                                      invention
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(MOLE-) INST MOLECULAR AGROBIOLOGY

Dong Y, Xu J;

Zhang L,

23-AUG-2000; 2000WO-SG00123

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Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance a disease in sustainable plant or animal and for reducing bacterial

The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The patching autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal by introducing a polynucleotide into a cell of such a plant or is useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A caterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.

This is the amino acid sequence of the autoinducer inactivation protein activity of which is studied in the Claim 17; Fig 9; 82pp; English. invention

250 AA; Sequence

120 180 240 240 EGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTP 120 121 IIVQRAEYEAAQHSEEYLKECILPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180 9 9 61 BGLFNGTFVBGQILPFMTEEDRIVNILKRVGYEPDDLLYIISSHLHFDHAGGNCAFTNTP EKSGPVILITIDASYTKENFENEVPFAGFDSELALSSIKRLKEVVMKEKPIVFFGHDIEQE 1 MTVKKLYFIPAGRCMLDHSSVNSALTBGKLLNLPVWCYLLETEEGPILVDTGMPESAVNN MIVKKLYFVPAGRCMLDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMPESAVNN Gaps .; 0 Length 250; Indels 91.4%; Score 1202; DB 23; 89.6%; Pred. No. 3.3e-122; ative 14; Mismatches 12; Best Local Similarity 89.6 Matches 224; Conservative : |:|||||| 241 KSCRVFPEYI 250 241 RGCKVFPEYI 250 Н Query Match 181 ð 셤 ò Q à g a à 셤 à

AAU78812 standard; Protein; 250 AA (first entry) 18-JUN-2002 Autoinducer AAU78812;

inactivation protein AiiK.

Autoinducer inactivation, AiiK, N-acyl-homoserine lactone, disease resistance, bacterial damage reduction, biofilm, potato soft rot disease; Erwinia carotovora,

Bacillus thuringiensis B25 WO200216623-A1.

28-FEB-2002

23-AUG-2000; 2000WO-SG00123

Autoinducer inactivation, AiiB; N-acyl-homoserine lactone, disease resistance; bacterial damage reduction; biofilm;

Autoinducer inactivation protein AiiB

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The invention describes an isolated polynuclectide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The autoinducer (N-acyl-homoserine lactone) inactivation protein. The colynuclectide is useful for increasing disease resistance in a plant or animal by introducing a polynuclectide into a cell of such a plant or animal by introducing a polynuclectide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein set useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A canimal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.

This is the amino acid sequence of the autoinducer inactivation protein activity of which is studied in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTVKKLYFVPAGRCMLDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMPESAVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EGLFNGTFVEGQILPKMTEEDRIVNILKRVGYEPDDLLYIISSHLHFDHAGGNGAFTNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                 Polynucleotide encoding autoinducer inactivation protein, bacterium having polynucleotide, and protein useful for increasing resistance a disease in sustainable plant or animal and for reducing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.3%; Score 1200; DB 23; Length 250; 90.0%; Pred. No. 5.4e-122; ive 12; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 AA
                                                                                                                                                                                                                                                    Claim 17; Fig 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU78815 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 90.0
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RGCKVFPEYI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 KĠĊRVFPĖYI 250
                                                                                                               WPI; 2002-304123/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AA;
                                                                                                                                   N-PSDB; ABK47476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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AAU78815
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monocytogenes protein #1475.

(first entry)

05-FEB-2002

ABB48771;

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Polymucleotide encoding autoinducer inactivation protein, bacterium having polymucleotide, and protein useful for increasing resistance a disease in sustainable plant or animal and for reducing bacterial
rot disease; Erwinia carotovora.
                                                                                              (MOLE-) INST MOLECULAR AGROBIOLOGY.
                                                                                                                                                                                         Claim 17; Fig 4; 82pp; English
               Agrobacterium tumefaciens M103
                                                              23-AUG-2000; 2000WO-SG00123
                                                                              23-AUG-2000; 2000WO-SG00123
                                                                                                             Xu J;
                                                                                                                             WPI; 2002-304123/34.
                                                                                                            Dong Y,
                                                                                                                                     N-PSDB; ABK47467.
                                WO200216623-A1
 soft
                                                28-FEB-2002
                                                                                                              Zhang L,
   potato
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tΩ

The invention describes an isolated polymucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The public is useful for increasing disease resistance in a plant or animal by introducing a polymucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein canimal, in a manner that allows the cell to express the gene. The protein content is useful for reducing bacterial damage to a plant or animal preferably thuman; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A canimal bacterium preferably Bacillus thuringiensis which is from B1, B2, B17, B18, B20, B21, B2 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by Erwinia carotovora. This is the amino acid sequence of the autoinducer inactivation protein animal is the autoinducer inactivation activity of which is studied in the invention.

263 AA; Sequence

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GLENGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTPI 121
                                                                                                                 170 TPGHOSLLIETEKSGPVILTIDASYTKENFENEVPFAGFDSEL--ALSSIKRLKEVVMKE 227
                                                                                                                                                                                                                    5 KLYFVPAG--RCMLDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMP-ESAVNNE 61
                                                                         62
                                                                    122 IVQRAEYEAAQHSEEYL-----KECILPNINYKIIEG---DYEVVPG---VQLLHTPGH
                          22;
 Length 263;
                          Indels
                          50; Mismatches 106;
23.7%; Score 311; DB 23; 32.1%; Pred. No. 4.3e-25;
                                                                                                                                                                                                                                                           228 KPIVFFGHDIEQERGCKVFPEY 249
                                                                                                                                                                                                                                                                                   240 DATVVTGHDPDAWANFKKAPEF 261
              32.1%;
                            84; Conservative
              Local Similarity
                                                                                                      62
                                                                                                                                63
  Query Match
                             Matches
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9

---NYKIIEG-----DYEVVPGVQLLHTPGHTPGHQSLLIETE 181

147

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ABB48771 standard; Protein; 283 AA.

RESULT 13 ABB48771 ID ABB48

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The present invention relates to the genome sequence of Listeria

CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
the are useful for selecting probes and primers for detecting genes in L.

CM monocytogenes and related organisms, and for studying genetic
monocytogenes and ther genome. The present invention. Proteins
capressed from the genome sequence of the present invention. Proteins
capressed from the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
controlled to the present invention of the minimit of the genome sequence and proteins encoded by it are also useful for
selecting compounds that regulate gene expression and cell replication
and modulate L. monocytogenes-related diseases. In addition, the genome
sequence and proteins encoded by it are also useful for
and modulate L. monocytogenes-related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
controlled to the treatment or prevention of infections by L.

CM monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LIDSGLGNRRLTEKOKRNYG-------VTEBSFVLEDLAQLSTAPEDIDYVLM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PNIRSKATY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                   Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 LVDTG-----MPESAVNNEGLFNGTFVEGQVLPKMTEEDRIVNILKRVGYEPEDLLYIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 SHLHFDHAGG------NGAFINTPIIVORAEYEAAQHSEEYLKECILPNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amend A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durant L;
                                                                                                                                                                                                                                                                                                                                                                                                                               C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux F Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, ernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A. T, Domann E, Hain T, Berche P, Charbit A, Durant L, J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                           Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Score 145.5; DB 23; Length 283; 25.5%; Pred No. 5.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID No 1476; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dussus,
Daniels J, Goeber ... Garrido-
Dominguez-Bernal G, Garrido-
Chakraborty T, Domann E, H
Perez-Diaz J, Baquero F, C
Maduenio E, De Pablos B, I
                                                                                                                                                                                                                                                                                                                    11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                          2000FR-0004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.1
Best Local Similarity 25.5
Matches 42, Conservative
                                                                                                                                                                                                    Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 AA;
                                                                                                                                                                                                                                         WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                              11-APR-2000;
                                                                                                                                                                                                                                                                               18-OCT-2001.
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea thydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigated.
Note: This patent is in the same patent family as WO200065062, which AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 RIVNILKRVGYEPEDLLYIISSHLHFDHAGGNGAFINTPIIVQRAEY----EAAQHSEEY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 LKECILP-----NLNYKIIEGDYBVVPG---VQLLHTPGHTPGHQSLLIETEKSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 I---ILSYYYGRRYDPHEVELKLEDGD-EIKVGKVKLRLIHTPGHTRGSSCLYYEEER-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 NSTLIPGELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKMTEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 MILMLEGVNLDSNV--YFLKSKDELLIVDTG-----TGVYWNKY----LDTARNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 141; DB 22; Length 222; 25.3%; Pred. No. 1.1e-06; Live 39; Mismatches 73; Indels 5:
Lecompte
                                                                                                                                                    Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                               Thierry JC, Prieur D, Dietrich J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 PVLLTIDASYTKENFENEVPFAGFDSELALSSIKRLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -IMFTGDTVFLGTYGRTDLPTGNEDK--IVESLELLK 192
                                                                                                                               Putative P. abyssi Zn-dependent hydrolase #4.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Pages 941-942; 1657pp; French
                                                                                                                                                                                                                                                                                (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                               AAB96283 standard; Protein; 222
                                                                                                                                                                                                                                        99FR-0005034.
                                                                                                                                                                                                                                                            99FR-0005034.
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-126236/14.
                                                                                                                                                                         Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 AA;
                                                                                                                                                                                                                                                                                                               Forterre P,
Querellou J,
                                                                                                                                                                                                                                        21-APR-1999;
                                                                                                                                                                                                                                                            21-APR-1999;
                                                                                                                                                                                             FR2792651-A1
                                                                                                          29-OCT-2001
                                                                                                                                                                                                                  27-OCT-2000
            160
                                                                                     AAB96283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                     AAB96283
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The invention relates to proteins (AAB73538-AAB73541) from Burkholderia cepacia which enhance the production of lipase, and the genes (AAH20219-AAH20222) encoding the lipase production-enhancing proteins. The genes of the invention were isolated from a 6.0 kb fragment of Burkholderia cepacia genomic DNA (AAH20223) which also concains the lipase (AAB73542). The invention also relates to expression cassettes, vectors, and transformants containing a gene of the invention and a lipase. The novel proteins and genes may be used in active compounds such as intermediates for drugs and agricultural chemicals. The production of lipase, which is for the preparation of optically chemicals. The present sequence represents a Burkholderia cepacia SC-20 lipase production-enhancing protein, designated OrfC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 EDLLYIISSHLHFDHAGG--NG---AFINTPIIVQRAEYEAAQHSEEYLKECILPNLNY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IEGDYEVVPGVQLLHTPGHTPGHQSLLIETEKSGPVLLTIDASYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 CYLLETEEGPILVDTGMPESAVNNEGLFNGTFVE--GQVLPKMTEEDRIVNILKRVGYEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipase-production enhancing gene, used to produce lipase, for use i
the preparation of optically active compounds as intermediates for
drugs -
                                                                                                                                                                                                                      Burkholderia cepacia lipase production-enhancing protein, OrfC.
                                                                                                                                                                                                                                                                               Lipase production-enhancing protein; strain SC-20; OrfC; open reading frame; expression cassette; vector; transformant; drug intermediate production; agricultural chemical production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%; Score 135.5; DB 22; Length 25.2%; Pred. No. 6.3e-06; Live 28; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 HIQIQRPEVSIAFDHDASLAAATRSRLLDQVSSE 249
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                          AAB73541 standard; Protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 4-6; 31pp; Japanese.
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                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia cepacia.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2001008683-A.
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                                                                                                                                                   07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2001
                                                                                          AAB73541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
AAB73541
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